

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2005, 22:30:27 ; Search time 207 Seconds
(without alignments)
3052.303 Million cell updates/sec

Title: US-10-511-559-73

Perfect score: 7693

Sequence: 1 ATRRRYLGAVLESLSDVWQSD.....MWHQIALRMEVLGCEADLY 1438

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378761 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	7693	100.0	1438	7 ADM75983	Adm75983 Wild-type
2	7693	100.0	1457	2 AAW46246	Aaw46246 Human fac
3	7693	100.0	1457	2 AAW44372	Aaw44372 Human fac
4	7693	100.0	1457	8 ADU47569	Adu47569 Human fac
5	7688	99.9	1438	7 ADM75988	Adm75988 Modified
6	7688	99.9	1438	7 ADM75985	Adm75985 Modified
7	7688	99.9	1438	7 ADM75989	Adm75989 Modified
8	7688	99.9	1438	7 ADM75984	Adm75984 Modified
9	7687	99.9	1438	7 ADM75986	Adm75986 Modified
10	7684	99.9	1438	3 ADM75987	Adm75987 Modified
11	7684	99.9	1438	3 AAB01262	Aab01262 B-domain
12	7684	99.9	1438	7 ADF31316	Adf31316 Variant o
13	7684	99.9	1457	2 AAY21675	Aay21675 Beta-doma
14	7684	99.9	1457	2 ADM98124	Adm98124 Human fac
15	7679.5	99.8	1464	8 ADU47624	Adu47624 Human fac
16	7676	99.8	1471	8 ADU47625	Adu47625 Human fac
17	7672	99.7	1479	8 ADU47617	Adu47617 Human fac
18	7668.5	99.7	1440	2 AAR12971	Aar12971 Factor VI
19	7667	99.7	1471	2 AAW23414	Aaw23414 Human B-d
20	7667	99.7	1471	4 AAB67959	Aab67959 Amino aci
21	7666	99.6	1471	8 ADU47608	Adu47608 Human fac
22	7637	99.3	1455	8 ADU47609	Adu47609 Human fac
23	7637	99.3	1461	8 ADU47616	Adu47616 Human fac
24	7635	99.2	1459	4 AAE10832	Aae10832 Human fac

25	7627.5	99.1	1568	8 ADU47621	Adu47621 Human fac
26	7625	99.1	1440	8 ADQ37592	Adq37592 Human fac
27	7625	99.1	1459	4 AAE10833	Aae10833 Human fac
28	7622	99.1	1459	4 AAE10827	Aae10827 Human fac
29	7620.5	99.1	1516	1 AAP80265	Aap80265 Modified
30	7619	99.0	1585	8 ADU47607	Adu47607 Human fac
31	7619	99.0	1585	8 ADU47613	Adu47613 Human fac
32	7614.5	99.0	1447	8 ADQ37595	Adq37595 Human fac
33	7614	99.0	1428	8 ADQ37589	Adq37589 Human fac
34	7614	99.0	1440	8 ADQ37607	Adq37607 Human fac
35	7610	98.9	1453	8 ADU47619	Adu47619 Human fac
36	7604.5	98.8	1450	8 ADU47615	Adu47615 Human fac
37	7603.5	98.8	1437	8 ADQ37593	Adq37593 Human fac
38	7603.5	98.8	1447	8 ADQ37610	Adq37610 Human fac
39	7603	98.8	1428	8 ADQ37604	Adq37604 Human fac
40	7603	98.8	1444	8 ADQ37596	Adq37596 Human fac
41	7603	98.8	1457	8 ADU47622	Adu47622 Human fac
42	7601	98.8	1424	4 AAB48842	Aab48842 Mutant ma
43	7601	98.8	1424	5 AAO18622	Aao18622 Human mat
44	7601	98.8	1424	9 ADZ65051	Adz65051 Human mat
45	7599.5	98.8	1441	8 ADQ37597	Adq37597 Human fac

ALIGNMENTS

RESULT 1
ID ADM75983 standard; protein; 1438 AA.
XX
AC ADM75983;
XX
DT 03-JUN-2004 (first entry)
XX
DE Wild-type B-domain deleted human FVIII protein sequence.
XX
KW human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
KW MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.
XX
OS Homo sapiens.
XX
PN WO2003087161-A1.
XX
PD 23-OCT-2003.
XX
PF 17-APR-2003; 2003WO-EP004063.
XX
PR 18-APR-2002; 2002EP-00008712.
PR 24-MAR-2003; 2003EP-00006554.
XX
PA (MERRE) MERCK PATENT GMBH.
PI Jones T, Baker M, Carr FJ;
XX
XX WPI; 2003-845307/78.
XX
PT New modified human Factor VIII molecule being substantially non-
PT immunogenic or less immunogenic than non-modified human Factor VIII,
PT useful in preparing a composition for treating e.g., Gaucher's disease.
XX
PS Disclosure; Fig 10; 68pp; English.
XX
CC The invention relates to a novel modified human Factor VIII molecule. The
CC modified human Factor VIII molecule being substantially non-immunogenic
CC or less immunogenic than a non-modified human Factor VIII and having
CC essentially the same biological specificity and activity when used in
CC vivo. The modified human Factor VIII molecule comprises specifically
CC altered amino acid residues compared with the non-modified parental
CC molecule, where the altered amino acid residues cause a reduction or an
CC elimination of one or more of the T-cell epitopes, which act in the
CC stimulatory non-modified molecule as MHC class II binding ligands and
CC stimulate T-cells. The potential of the modified Factor VIII molecule is
CC useful for the manufacture of the modified Factor VIII molecule or a

CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.
 CC The modified Factor VIII molecule is useful in preparing a composition
 CC for treating e.g., Gaucher's disease. This sequence represents a wild-
 CC type B-domain deleted human FVIII protein sequence of the invention.

XX Sequence 1438 AA:

Query Match 100.0%; Score 7693; DB 7; Length 1438;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATRRYVIGAVLSMDYQSDLGELPVDAFRPPRPKSPFNTSVYKKTLFVETDHLFN 60
DB 1 ATRRYVIGAVLSMDYQSDLGELPVDAFRPPRPKSPFNTSVYKKTLFVETDHLFN 60
QY 61 IAKRRPMMGLIGFTIOAEVYDTVVITLKNNASHPVSLHAGVGYWKAEGAEVDDOTSQ 120
DB 61 IAKRRPMMGLIGFTIOAEVYDTVVITLKNNASHPVSLHAGVGYWKAEGAEVDDOTSQ 120
QY 121 REKEDDKVFPGGSHTYWQVLKENGPMASDPLCTYSYLSHVDLVKDLNSGLIGALLVCR 180
DB 121 REKEDDKVFPGGSHTYWQVLKENGPMASDPLCTYSYLSHVDLVKDLNSGLIGALLVCR 180
QY 121 REKEDDKVFPGGSHTYWQVLKENGPMASDPLCTYSYLSHVDLVKDLNSGLIGALLVCR 180
DB 121 REKEDDKVFPGGSHTYWQVLKENGPMASDPLCTYSYLSHVDLVKDLNSGLIGALLVCR 180
QY 181 EGSIAKETOTLHAFILLFVAFDGGKSHSTKNSLMODRDAASARAPKMTNGVYNR 240
DB 181 EGSIAKETOTLHAFILLFVAFDGGKSHSTKNSLMODRDAASARAPKMTNGVYNR 240
QY 241 SLPGIGCHRSKSYVWHVIGMTPEVHSIFLEGHTFLVRNHRQASLEISPTFTTAQTLL 300
DB 241 SLPGIGCHRSKSYVWHVIGMTPEVHSIFLEGHTFLVRNHRQASLEISPTFTTAQTLL 300
QY 301 MDLQGFLLFCHISSHQHDGMEAYVKVDSCPREPQLRMKNNEABDYDDLTDSEMDVVR 360
DB 301 MDLQGFLLFCHISSHQHDGMEAYVKVDSCPREPQLRMKNNEABDYDDLTDSEMDVVR 360
QY 361 DDNDSPFTIQIRSAVAKKPKTWVHYIAAEEEDMVAAPLVLPDRSRYSQYLNNGPORIG 420
DB 361 DDNDSPFTIQIRSAVAKKPKTWVHYIAAEEEDMVAAPLVLPDRSRYSQYLNNGPORIG 420
QY 421 RKYKVRPMAYTDEFTKREAIQHESGILGPLVGEVDDTLIIFFKQASRPYNIYPHG 480
DB 421 RKYKVRPMAYTDEFTKREAIQHESGILGPLVGEVDDTLIIFFKQASRPYNIYPHG 480
QY 481 TDVAPLYSRRLPKGVKHLKDFPILPGELFKYKWTVVEDGPTKSDPRCLTRYSSPVNME 540
DB 481 TDVAPLYSRRLPKGVKHLKDFPILPGELFKYKWTVVEDGPTKSDPRCLTRYSSPVNME 540
QY 541 RDLASGLIGPLLCYKESVDQRGNQMSDKNNVLLFSVFDNRSMWYLTENIQRLPNPAG 600
DB 541 RDLASGLIGPLLCYKESVDQRGNQMSDKNNVLLFSVFDNRSMWYLTENIQRLPNPAG 600
QY 601 VQLEDPERFQASINMHSINGVYFDSLQSLVCLAEVAYWYIISIGQTFPLSVFFGYTFKH 660
DB 601 VQLEDPERFQASINMHSINGVYFDSLQSLVCLAEVAYWYIISIGQTFPLSVFFGYTFKH 660
QY 661 KMVYEDTLTLFPFSGEIVFMSMENPGLMIILGCHNSDFRNRGMTALLKVSQCKNTGDIYE 720
DB 661 KMVYEDTLTLFPFSGEIVFMSMENPGLMIILGCHNSDFRNRGMTALLKVSQCKNTGDIYE 720
QY 721 DSYEDISAYILSKNNATEPFSFSONPVLKHOIREITRTTQSOOEEDVDYDITSVEMKK 780
DB 721 DSYEDISAYILSKNNATEPFSFSONPVLKHOIREITRTTQSOOEEDVDYDITSVEMKK 780
QY 781 EDPIIYEDENQSPRSFOKTRHAFIAAVERLMDYGMSSPHVLRNRAQSSGVQPFKKV 840
DB 781 EDPIIYEDENQSPRSFOKTRHAFIAAVERLMDYGMSSPHVLRNRAQSSGVQPFKKV 840
QY 841 FOEFTDGSFTQPLVYRGELNEHGLGPYIRAEVEDNIVWTRNOASRPYSYSSLLSYEE 900
DB 841 FOEFTDGSFTQPLVYRGELNEHGLGPYIRAEVEDNIVWTRNOASRPYSYSSLLSYEE 900
QY 901 DORGAERKRVVFNETKTYFMKVQHMMATPTXBEFCDKAAAYSDVDLECVHSGILGP 960
DB 901 DORGAERKRVVFNETKTYFMKVQHMMATPTXBEFCDKAAAYSDVDLECVHSGILGP 960

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DB 901 DORGAERKRVVFNETKTYFMKVQHMMATPTXBEFCDKAAAYSDVDLECVHSGILGP 960
QY 961 LVCHNTNLNPAHGRQVTVQEFALFTIPEDETSWYFTENBERNCRAPCINQMEDPFXE 1020
DB 961 LVCHNTNLNPAHGRQVTVQEFALFTIPEDETSWYFTENBERNCRAPCINQMEDPFXE 1020
QY 1021 NYRPHAINGYIMDTLPGLVMAODQIRWYILMSGNENIHSIHPSGHVFTVRKKEEYKMA 1080
DB 1021 NYRPHAINGYIMDTLPGLVMAODQIRWYILMSGNENIHSIHPSGHVFTVRKKEEYKMA 1080
QY 1081 LVNLYPGVEFTVWMLPSKAGIMRVECLIGEHILHAGASTFLVYVSNCCQPLGMASSGHIRD 1140
DB 1081 LVNLYPGVEFTVWMLPSKAGIMRVECLIGEHILHAGASTFLVYVSNCCQPLGMASSGHIRD 1140
QY 1141 FOITTAGQYQOMAPKLARLHYSGSINAWSTKEPFSMIKVYDLAPMIIHGIXTQAGARQFS 1200
DB 1141 FOITTAGQYQOMAPKLARLHYSGSINAWSTKEPFSMIKVYDLAPMIIHGIXTQAGARQFS 1200
QY 1201 SLVYSQFIIMYSIDGKKWQTYRGNSTGTLMPFGVNDSSGINKININPPIIARYIRLHPT 1260
DB 1201 SLVYSQFIIMYSIDGKKWQTYRGNSTGTLMPFGVNDSSGINKININPPIIARYIRLHPT 1260
QY 1261 HYSIRSTLRWELMGCDLNSCMLGMSKRAISDAQITASSYFTNNMPTWSPSKARLHLOG 1320
DB 1261 HYSIRSTLRWELMGCDLNSCMLGMSKRAISDAQITASSYFTNNMPTWSPSKARLHLOG 1320
QY 1321 RSNAMPQVNNPKEMIQVDFQKTMKYTGVTQGVKSLTSMVYKEFLISSQDGHQWTLF 1380
DB 1321 RSNAMPQVNNPKEMIQVDFQKTMKYTGVTQGVKSLTSMVYKEFLISSQDGHQWTLF 1380
QY 1381 FQNGKRVVFOGNDSTFPVYVNSLDPLLTRYLRIHQSVYHQIALKMEVLCGEADLY 1438
DB 1381 FQNGKRVVFOGNDSTFPVYVNSLDPLLTRYLRIHQSVYHQIALKMEVLCGEADLY 1438

RESULT 2
AAW46246
ID AAW46246 standard; protein; 1457 AA.
AC AAW46246;
XX
DT 25-MAR-2003 (revised)
DT 06-AUG-1998 (first entry)
XX
DE Human factor VIII beta-domain deleted SQN deletion protein sequence.
XX
KW Replication defective; recombinant retrovirus; RRV; therapeutic protein;
KW hemophilia; thrombosis; hypercoagulable disorder; liver disease; human;
KW hepatitis; thalassemia; phenylketonuria; Leisch-Nyhan syndrome; diabetes;
KW cystic fibrosis; Duchenne's Muscular Dystrophy; hypercholesterolemia;
KW hypopituitarism; adenine deaminase deficiency; HIV infection; anemia;
KW Gaucher's syndrome; high blood pressure; Alzheimer's disease; autoimmune;
KW inflammatory disease; factor VIII.
XX
OS Homo sapiens.
PN MO9800541-A2.
PN
PD 08-JAN-1998.
XX
PE 02-JUL-1997; 97MO-US011784.
XX
PR 03-JUL-1996; 96US-00645601.
PR 13-AUG-1996; 96US-00696381.
PR 04-JUN-1997; 97US-00869309.
XX
PA (CHIR ) CHIRON CORP.
PI Jolly DJ, Barber JR, Chang SMW, Respass JG, Allen JR, Boder M;
PI Chong K, De La Vega D, Depolo NJ, Heu DC, Ibanez CE;
PI Mittelstaedt DM, Prusaak CE, Greengard J, Lee R;
XX WPI; 1998-086966/08.

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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: November 25, 2005, 22:33:30 ; Search time 53 Seconds

(without alignments)
2610.560 million cell updates/sec

Title: US-10-511-559-73

Perfect score: 7693

Sequence: 1 ATRRYVLGAVELSMVDVQSD.....MWHQIALRMEVLGCEADLY 1438

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_80:*

2: PIR1:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7236	94.1	2351	1 E2HU	coagulation factor
2	6236	81.1	2133	2 T42763	coagulation factor
3	6201	80.6	2319	2 A47004	coagulation factor
4	2391.5	31.1	2224	1 KFHUS	coagulation factor
5	2371	30.8	2183	2 T42764	coagulation factor
6	2370	30.8	2211	1 KPBOS	coagulation factor
7	1740.5	22.6	1069	1 KTHU	ferroxidase (EC 1.1.1.1)
8	1696.5	22.1	1059	1 A45210	ferroxidase (EC 1.1.1.1)
9	1104	14.4	216	2 A4258	factor VIII-associated protein
10	663	8.6	427	1 A36479	protein precursor
11	657	8.5	463	1 A36479	protein precursor
12	650	8.4	409	2 T11743	protein precursor
13	635	8.3	401	2 S65138	protein precursor
14	635	8.3	427	2 A25945	protein precursor
15	543	7.1	869	2 A25945	protein precursor
16	443	5.8	927	1 J00948	protein precursor
17	424.5	5.5	218	2 A47285	protein precursor
18	306.5	4.0	3133	2 S52093	protein precursor
19	262	3.4	845	2 A49508	protein precursor
20	221	2.9	719	2 S51736	protein precursor
21	211	2.7	1283	2 T13799	protein precursor
22	207.5	2.7	737	2 T1349	protein precursor
23	206.5	2.7	737	2 T15615	protein precursor
24	193	2.5	913	2 A48280	protein precursor
25	192	2.5	876	2 A49508	protein precursor
26	185.5	2.4	855	2 S42621	protein precursor
27	185.5	2.4	910	2 A53137	protein precursor
28	173.5	2.3	819	2 I48859	protein precursor
29	171	2.2	1381	2 T31083	protein precursor

30	171	2.2	1385	2 T14158	neurexin IV - mouse
31	149.5	1.9	578	2 S66353	L-ascorbate oxidase
32	149	1.9	1883	2 G82875	hypothetical protein
33	148	1.9	632	2 S62580	probable multicop
34	141.5	1.8	1156	2 S46430	botulinum neurotoxin
35	140.5	1.8	1196	2 JQ1467	toxin, nontoxic co
36	140.5	1.8	1217	2 T18209	nmug protein - Bac
37	139	1.8	1193	2 JC4901	nontoxic-nonhemag
38	137.5	1.8	580	2 F84828	probable lactase (
39	137.5	1.8	903	2 F82080	preprotein translo
40	136.5	1.8	2657	2 T18497	hypothetical prote
41	135	1.8	343	2 T35030	probable copper ox
42	134.5	1.7	791	2 T16031	hypothetical prote
43	134.5	1.7	1132	2 H82887	hypothetical prote
44	133.5	1.7	567	2 T44928	L-ascorbate oxidase
45	133.5	1.7	2925	2 T00133	RNA-directed RNA p

ALIGNMENTS

RESULT 1

E2HU
coagulation factor VIII precursor [validated] - human
N:Alternate names: antihemophilic factor A; coagulation factor VIIIc; procoagulant compo
C:Species: Homo sapiens (man)
C>Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text change 31-Dec-2004
C:Accession: I54318; A00525; I58059; A23584; A26174; A42348; A43986; S63527; S66445; B426
R:Giltisler, J.; Wood, W.I.
Hum. Mol. Genet. 1, 199-200, 1992
A:Title: Sequence of the exon-containing regions of the human factor VIII gene.
A:Reference number: I54318; MUID:93265012; PMID:1303178
A:Accession: I54318
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1921, 'S', 1923-2351 <RES>
A:Cross-references: UNIPARC:UPI000012A416; EMBL:X01165; EMBL:X01166; EMBL:X01179
R:Toole, J.U.; Knopf, J.L.; Wozney, J.M.; Soltzman, L.A.; Buecker, J.L.; Pittman, D.D.; I
s, D.N.; Hewick, R.M.
Nature 312, 342-347, 1984
A:Title: Molecular cloning of a cDNA encoding human antihemophilic factor.
A:Reference number: I58059; MUID:85061550; PMID:6438528
A:Accession: I58059
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-74, 'V', 76-1259, 'E', 1261-2351 <RES>
A:Cross-references: UNIPARC:UPI0000144860; GB:X01740; NID:G182802; PIDN:AAA52484.1; PID:G
R:Truett, M.A.; Blacher, R.; Burke, R.L.; Caput, D.; Chu, C.; Dina, D.; Hartog, K.; Kuo, B.; Randolph, A.; Under, M.S.; Valenzuela, P.; Dahl, H.H.; Favaloro, J.; Hansen, J.; No
DNA 4, 333-349, 1985
A:Title: Characterization of the polypeptide composition of human factor VIII:C and the r
A:Reference number: A23584; MUID:86081164; PMID:3935400
A:Accession: A23584
A:Molecule type: mRNA
A:Residues: 1-2351 <TRU>
A:Cross-references: UNIPARC:UPI000012A416; GB:M4113; NID:G182817; PIDN:AAA52485.1; PID:G
R:Batoni, D.; Rodriguez, H.; Venar, G.A.
Biochemistry 25, 505-512, 1986
A:Title: Proteolytic processing of human factor VIII. Correlation of specific cleavages l
ity.
A:Reference number: A26174; MUID:66159740; PMID:3082357
A:Accession: A26174
A:Molecule type: protein
A:Residues: 20-36,392-399, 'X', 401-402,1668-1678,1709-1722, 'D', 1723-1725,1741-1755 <EAT>
A:Cross-references: UNIPARC:UPI0000172296; UNIPARC:UPI0000172297; UNIPARC:UPI0000172298;

R:Pltman, D.D.; Wang, J.H.; Kaufman, R.J.
Biochemistry 31, 3315-3325, 1992
A:Title: Identification and functional importance of tyrosine sulfate residues within re
A:Reference number: A42348; PMID:92207952; PMID:1554716
A:Accession: A42348
A:Molecule type: Protein
A:Residues: 20-36/356-37/392-408/582-594/1668-1669, 'X', 1671/1672-1692/1693-1708/1709-17
A:Cross-references: UNIPARC:UPI0000172296; UNIPARC:UPI000017229B; UNIPARC:UPI000017229C;
2A1
A:Experimental source: recombinant material from Chinese hamster ovary cells
A>Note: sequence extracted from NCBI backbone and corrected to correspond with the publi
R:Ray, P.U.; Smudzin, T.M., 1989
J. Biol. Chem. 264, 14005-14010, 1989
A:Title: Interubiquitin fluorescence energy transfer in human factor VIII.
A:Reference number: A43986; PMID:89340500; PMID:2503509
A:Accession: A43986
A:Molecule type: protein
A:Residues: 'X', 517-523/1853-1860, 'X', 1862-1864, 'X', 1866 <FAY>
A:Cross-references: UNIPARC:UPI00001722A2; UNIPARC:UPI00001722A3
R:Leyte, A.; van Schijndel, H.B.; Niehrs, C.; Hutterer, W.B.; Verbeet, M.P.; Mertens, K.;
J. Biol. Chem. 266, 740-746, 1991
A:Title: Sulfation of Tyr(1680) of human blood coagulation factor VIII is essential for
A:Reference number: A56109; PMID:91093266; PMID:1896735
A:Contents: annotation; sulfation
R:Gleicher, J.; Wood, W.I.; Goralka, T.M.; Wion, K.L.; Chen, E.Y.; Eaton, D.H.; Vohar,
Nature 312, 326-330, 1984
A:Title: Characterization of the human factor VIII gene.
A:Reference number: A56196; PMID:85061547; PMID:6438525
A:Contents: annotation; introns
R:McMullen, B.W.; Fujikawa, K.; Davie, E.W.; Hedner, U.; Ezban, M.
Protein Sci. 4, 740-746, 1995
A:Title: Locations of disulfide bonds and free cysteines in the heavy and light chains c
A:Reference number: A56216; PMID:95338127; PMID:7613471
A:Contents: annotation; disulfide bonds
A>Note: 329-Cys, 711-Cys, and 2019-Cys were shown to have free sulfhydryls
R:Kjake, M.; Hedner, A.; Talbo, G.; Persson, E.; Thomsen, J.; Ezban, M.
Eur. J. Biochem. 234, 773-779, 1995
A:Title: Amino acid residues 721-729 are required for full factor VIII activity.
A:Reference number: S63527; PMID:96163459; PMID:8575434
A:Accession: S63527
A:Molecule type: protein
A:Residues: 733-752/753-759 <KUA>
A:Cross-references: UNIPARC:UPI00001722A4; UNIPARC:UPI00001722A5
R:Lind, P.; Larsson, K.; Sjötra, J.; Sydow-Baeckman, M.; Almerdt, A.; Gray, E.; Sandberg
Eur. J. Biochem. 232, 19-27, 1995
A:Title: Novel forms of B-domain-deleted recombinant factor VIII molecules. Construction
A:Reference number: S66445; PMID:96048024; PMID:7356150
A:Accession: S66445
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1668-1685 <LIN>
A:Cross-references: UNIPARC:UPI00001722A6
C:Comment: Factor VIII is activated by factor Xa and thrombin, but prolonged exposure pr
C:Genetics:
A:Gene: GDB:F8C
A:Cross-references: GDB:119124; OMIM:306700
A:Map position: Xq28-Xq28
A:Positions: 48/2; 89/1; 130/1; 201/1; 224/1; 263/1; 337/1; 424/2; 481/3; 513/1; 584/3; 63
C:Function:
A:Description: acts as a cofactor, with calcium and phospholipid, for the factor IXa pro
A:Pathway: blood coagulation
C:Superfamily: coagulation factors V/VIII; discoidin I amino-terminal homology; ferroxid
C:Keywords: acute phase; blood coagulation; duplication; glycoprotein; hemophilia A; pla
F:1-19/Domin: signal sequence #statue predicted <SIG>
F:20-2351/Product: coagulation factor VIII #statue experimental <MAT>
F:20-740/Product: coagulation factor VIII heavy chain #statue experimental <ACH>
F:20-356/Domin: A1 <DA1>
F:23-348/Domin: A1 <DA1>
F:392-759/Domin: A2 <DA2>
F:402-759/Domin: A2 <DA2>
F:760-1667/Domin: B <DBO>
F:1668-3351/Product: coagulation factor VIIa light chain #statue experimental <ACL>
F:1709-2038/Domin: A3 <DA3>

F:1716-2038/Domin: ferroxidase repeat homology <FO3>
F:2039-2191/Domin: C1 <DC1>
F:2039-2198/Domin: discoidin I amino-terminal homology <DN1>
F:2192-2351/Domin: C2 <DC2>
F:2192-2345/Domin: discoidin I amino-terminal homology <DN2>
F:60-258, 601, 776, 803, 847, 919, 962, 1020, 1024, 1074, 1085, 1204, 1274, 1278, 1301, 1319, 1403, 1
F:172-198, 267-348, 547-573, 649-730, 1851-1877, 1918-1922, 2040-2188/Disulfide bonds: #statu
F:355-356/Cleavage site: Arg-Met (coagulation factor Xa, protein C) #status predicted
F:365, 737, 738, 742, 1683, 1699/Binding site: sulfate (Tyr) (covalent) #status experimental
F:391-392/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experimental
F:414, 426/Binding site: sulfate (Tyr) (covalent) #status predicted
F:759-760/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experimental
F:1667-1668/Cleavage site: Arg-Glu (unidentified proteinase) #status experimental
F:1708-1709/Cleavage site: Arg-Ala (coagulation factor Xa, thrombin) #status experimental
F:1740-1741/Cleavage site: Arg-Ala (coagulation factor Xa) #status experimental
F:2193-2345/Disulfide bonds: #status predicted

Query Match 94.1%; Score 7236; DB 1; Length 2351;
Best local similarity 61.7%; Pred. No. 0;
Matches 1438; Conservative 0; Mismatches 0; Indels 894; Gaps 1;

Qy 1 ATRRYVIGAVELSDVYQWQSLGELPVNARPPRPKSPFPPTSVYKKTLFVETDHLFN 60
Db 20 ATRRYVIGAVELSDVYQWQSLGELPVNARPPRPKSPFPPTSVYKKTLFVETDHLFN 79
Qy 61 IAKRPMPMGLIGPTIAGVYDVTVITLKNMASHPVSLHAGVYMKASBGAEDDQTSQ 120
Db 80 IAKRPMPMGLIGPTIAGVYDVTVITLKNMASHPVSLHAGVYMKASBGAEDDQTSQ 139
Qy 121 REKEDRVFPQSGHTVYVQVLEKGNMADPLCTYSYLSHVDLVKDLNSGLIGALLVCR 180
Db 140 REKEDRVFPQSGHTVYVQVLEKGNMADPLCTYSYLSHVDLVKDLNSGLIGALLVCR 199
Qy 181 EGSIAKKTQTLKHTLLFVPEGKSWHSETKSLMODDASARMPKHTNGVYNR 240
Db 200 EGSIAKKTQTLKHTLLFVPEGKSWHSETKSLMODDASARMPKHTNGVYNR 259
Qy 241 SLPLGICHRKSYVWHVIGKTPPEVHSIFLEGHTPLVRNHRQASLEISPTFLTAOTIL 300
Db 260 SLPLGICHRKSYVWHVIGKTPPEVHSIFLEGHTPLVRNHRQASLEISPTFLTAOTIL 319
Qy 301 MDLGQFLPLFCHISSHQDGEAVYKVDSCPEEPQLRMKNNEBARDYDDTLTDSMDVVR 360
Db 320 MDLGQFLPLFCHISSHQDGEAVYKVDSCPEEPQLRMKNNEBARDYDDTLTDSMDVVR 379
Qy 361 DDNSPSFQIGIRSAKKGPTWYVYIAEEDMDVAPLVLPDRSYKSOYLNNGPORIG 420
Db 380 DDNSPSFQIGIRSAKKGPTWYVYIAEEDMDVAPLVLPDRSYKSOYLNNGPORIG 439
Qy 421 RYKRVFPMAYDTBFTFTRBAIQHESGILGPLLYGEVDTLLIFKQASRPVNIYPHGI 480
Db 440 RYKRVFPMAYDTBFTFTRBAIQHESGILGPLLYGEVDTLLIFKQASRPVNIYPHGI 499
Qy 481 TDVRLVSRRLPKGVKHLKDFPLPGELIFRYKWTVVEDGPTKSDPRCLTRYSSPVNME 540
Db 500 TDVRLVSRRLPKGVKHLKDFPLPGELIFRYKWTVVEDGPTKSDPRCLTRYSSPVNME 559
Qy 541 RDLASGLIGPLLCYKSSVQDRQNMDSKRNVLTFVPEPNRHWYLTENIQRLLPNAG 600
Db 560 RDLASGLIGPLLCYKSSVQDRQNMDSKRNVLTFVPEPNRHWYLTENIQRLLPNAG 619
Qy 601 VQLEDPEFOASNIHMSINGVYFDSLQVCLHEAVYVYISIGQDTFLSVFSGGYTFKH 660
Db 620 VQLEDPEFOASNIHMSINGVYFDSLQVCLHEAVYVYISIGQDTFLSVFSGGYTFKH 679
Qy 661 KMYVEDTLTLFPFSGETVFMSPENGLWILGCHNSDFRNGMTALLKVSXCDKXTGDIYE 720
Db 680 KMYVEDTLTLFPFSGETVFMSPENGLWILGCHNSDFRNGMTALLKVSXCDKXTGDIYE 739
Qy 721 DSYEDISAYLLSKNALEPSSF----- 742
Db 740 DSYEDISAYLLSKNALEPSSF----- 759

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OM protein - protein search, using sw model

Run on: November 25, 2005, 22:32:09 ; Search time 270 Seconds
(without alignments)
3757.591 Million cell updates/sec

Title: US-10-511-559-73

Perfect score: 7693
Sequence: 1 ATRRYILGAVELSDWYQSD.....WHQIALRMVELGCEADPLY 1438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7236	94.1	2351	1	PA8_HUMAN
2	7236	94.1	2351	1	Q5H769_HUMAN
3	7236	94.1	2351	1	PA8_CANFA
4	6236	81.1	2133	1	PA8_PIG
5	6201	80.6	2319	1	PA8_MOUSE
6	4967.5	64.6	2258	2	Q7N966_RAT
7	3236	42.1	1639	2	Q804W6_FUGRU
8	2672.5	34.7	1459	2	Q593B6_PSETE
9	2652	34.5	1460	2	Q7S2N0_PSETE
10	2650.5	34.5	1460	2	Q58191_OXYRANUS
11	2631	34.2	1460	2	Q58190_OXYRANUS
12	2542	33.0	1802	2	Q804W5_FUGRU
13	2490.5	32.4	2119	2	Q90X47_BRARE
14	2394.5	31.1	2224	2	PA8_HUMAN
15	2387.5	31.0	2224	2	Q5R347_HUMAN
16	2380	30.9	1304	2	Q4RPE7_TETNG
17	2375	30.9	2229	2	Q5R346_HUMAN
18	2371	30.8	2183	2	Q88783_MOUSE
19	2370	30.8	2211	2	PA5_BOVIN
20	2355.5	30.6	2258	1	PA5_PIG
21	2326.5	30.2	1377	2	Q804X3_CHICK
22	2093	23.5	1157	1	HEBP_MOUSE
23	1809	23.3	1157	1	HEBP_MOUSE
24	1793	22.8	1158	1	HEBP_HUMAN
25	1751	22.8	1158	1	HEBP_HUMAN
26	1751	22.8	1158	1	HEBP_HUMAN
27	1740	22.6	1087	2	Q7ZU12_BRARE
28	1739	22.6	1087	2	Q6P3G1_BRARE
29	1736.5	22.6	1065	1	CERU_HUMAN
30	1718.5	22.3	1084	2	Q9JL57_RAT
31	1696	22.0	1048	2	Q4T829_TETNG

32	1693.5	22.0	1059	1	CERU_RAT	P13635	rattus norv
33	1684	21.9	1061	2	Q6P5C8_MOUSE	Q6P5C8	mus musculus
34	1644.5	21.4	1062	1	CERU_MOUSE	Q61447	mus musculus
35	1627	21.1	1048	2	Q9XT27_SHEEP	Q9XT27	ovis aries
36	1601.5	20.8	349	2	Q684Q7_MOUSE	Q684Q7	mus musculus
37	1599.5	20.8	2102	2	Q7TPK2_RAT	Q7TPK2	rattus norv
38	1589.5	20.7	1007	2	Q4SPU7_TETNG	Q4SPU7	tetradodon n
39	1543.5	20.1	355	2	Q8BQ43_MOUSE	Q8BQ43	mus musculus
40	1443.5	18.8	745	2	Q804X4_CHICK	Q804X4	gallus galli
41	1341	17.4	891	2	Q5JUI1_HUMAN	Q5JUI1	homo sapien
42	1183.5	15.4	811	2	Q5JZ08_HUMAN	Q5JZ08	homo sapien
43	1104	14.4	216	2	Q14286_HUMAN	Q14286	homo sapien
44	1078	14.0	248	2	Q5RAM1_PONNY	Q5RAM1	pongo pygma
45	1046.5	13.6	626	2	Q90ZT2_BRARE	Q90ZT2	brachydanio

ALIGNMENTS

RESULT 1	PA8_HUMAN	STANDARD	PRT: 2351 AA.
AC	P00451		
DT	21-JUN-1986 (Rel. 01, Created)		
DT	21-JUN-1986 (Rel. 01, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		
DE	Coagulation factor VIII precursor (Procoagulant component)		
DE	(Antihemophilic factor) (AHF) [Contains: Factor VIIIa heavy chain, 200 kDa isoform; Factor VIIIa heavy chain, 92 kDa isoform; Factor VIII B chain; Factor VIIIa light chain].		
GN	Name=F8; Synonyms=F8C;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE [MRNA].		
RX	MEDLINE=86081164; PubMed=3935400;		
RA	Truett M.A., Blacher R., Burke R.L., Caput D., Chu C., Dina D.,		
RA	Hatog K., Kuo C.H., Mestarz F.R., Merryweather J.P., Najarian R.,		
RA	Pachl C., Potter S.J., Puma J., Quiroga M., Rall L.B., Randolph A.,		
RA	Urdea M.S., Valenzuela P., Dahl H.-H.M., Favalaro J., Hansen J.,		
RA	Nordfang O., Ezban M.;		
RT	"Characterization of the polypeptide composition of human factor VIII:C and the nucleotide sequence and expression of the human kidney		
RT	cDNA.";		
RL	DNA 4:333-349(1985).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE [MRNA].		
RX	MEDLINE=85061548; PubMed=6438526;		
RA	Wood W.I., Capon D.J., Simonsen C.C., Eaton D.L., Gitschier J.,		
RA	Key B., Seeburg P.H., Smith D.H., Hollingshead P., Wion K.L.,		
RA	DeWalt E., Tuddenham E.G.D., Venar G.A., Lawn R.M.;		
RT	"Expression of active human factor VIII from recombinant DNA clones.";		
RL	Nature 312:330-337(1984).		
RN	[3]		
RP	NUCLEOTIDE SEQUENCE [MRNA].		
RX	MEDLINE=85061550; PubMed=6438528;		
RA	Tooze J.J., Knopf J.L., Wozney J.M., Sultzman L.A., Buecker J.L.,		
RA	Pitman D.D., Kaufman R.J., Brown E., Shoemaker C., Orr E.C.,		
RA	Amplett G.W., Foster W.B., Coe M.L., Knutson G.J., Fawcett D.N.,		
RA	Hewick R.M.;		
RT	"Molecular cloning of a cDNA encoding human antihemophilic factor.";		
RL	Nature 312:342-347(1984).		
RN	[4]		
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA].		
RX	MEDLINE=93265012; PubMed=1303178;		
RA	Gitschier J., Wood W.I.;		
RT	"Sequence of the exon-containing regions of the human factor VIII		
RL	Hum. Mol. Genet. 1:199-200(1992).		
RN	[5]		

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS GLU-1260 AND VAL-2257.
 RA Rieder M.J., Daniele R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
 RA Rajkumar N., Yi O., Nickerson D.A.;
 RT "SeattlesNP, NHLBI HL66682 program for genomic applications, UW-
 RT FHCC, Seattle, WA (URL: <http://pga.gs.washington.edu/>).";
 RL Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 2064-2070.
 RA de Water N.S., Williams R., Browett P.J.;
 RT "Factor VIII gene normal intron 20 sequence.";
 RL Submitted (Jun-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SULFATION OF TYR-1699.
 RX MEDLINE=91093266; PubMed=1698725;
 RA Leyte A., van Schijndel H.B., Niehrs C., Huttner W.B., Verbeet M.F.,
 RA Mertens K., van Mourik J.A.;
 RT "Sulfation of Tyr1680 of human blood coagulation factor VIII is
 RT essential for the interaction of factor VIII with von Willebrand
 RT factor.";
 RL J. Biol. Chem. 266:740-746(1991).
 RN [8]
 RP SULFATION.
 RX MEDLINE=92207952; PubMed=1554716;
 RA Pileman D.D., Wang J.H., Kaufman R.J.;
 RT "Identification and functional importance of tyrosine sulfate residues
 RT within recombinant factor VIII.";
 RL Biochemistry 31:3315-3325(1992).
 RN [9]
 RP DISULFATION SITES TYR-737, TYR-738 AND TYR 742, AND DISULFIDE BONDS.
 RX MEDLINE=9538127; PubMed=7613471;
 RA McWilliam B.A., Fujikawa K., Davie E.W., Hedner U., Ezban M.;
 RT "Locations of disulfide bonds and free cysteines in the heavy and
 RT light chains of recombinant human factor VIII (antihemophilic factor
 RT A).";
 RL Protein Sci. 4:740-746(1995).
 RN [10]
 RP STRUCTURE BY NMR OF 2322-2343.
 RX MEDLINE=95200924; PubMed=7693714;
 RA Gilbert G.E., Bajaj J.D.;
 RT "Membrane-binding peptide from the C2 domain of factor VIII forms an
 RT amphipathic structure as determined by NMR spectroscopy.";
 RL Biochemistry 34:3022-3031(1995).
 RN [11]
 RP REVIEW ON MOLECULAR BASIS OF HEMA.
 RX MEDLINE=91221499; PubMed=1902642;
 RA Gitschier J.;
 RT "The molecular basis of hemophilia A.";
 RL Ann. N. Y. Acad. Sci. 614:89-96(1991).
 RN [12]
 RP REVIEW ON MOLECULAR BASIS OF HEMA.
 RX MEDLINE=89088506; PubMed=2491949;
 RA White G.C. II, Shoemaker C.B.;
 RT "Factor VIII gene and hemophilia A.";
 RL Blood 73:1-12(1989).
 RN [13]
 RP REVIEW ON MOLECULAR BASIS OF HEMA.
 RX MEDLINE=95245332; PubMed=7728145;
 RA Antonarakis S.E., Kazazian H.H. Jr., Tuddenham E.G.D.;
 RT "Molecular etiology of factor VIII deficiency in hemophilia A.";
 RL Hum. Mutat. 5:1-22(1995).
 RN [14]
 RP VARIANT HEMA GLN-2326.
 RX MEDLINE=86235434; PubMed=3012775;
 RA Gitschier J., Wood W.I., Shuman M.A., Lawn R.M.;
 RT "Identification of a missense mutation in the factor VIII gene of a
 RT mild hemophilia.";
 RL Science 232:1415-1416(1986).
 RN [15]
 RP VARIANT HEMA PRO-2135.
 RX MEDLINE=88096539; PubMed=3122181;
 RA Levinson B., Janco R.L., Phillips J.A. III, Gitschier J.;
 RT "A novel missense mutation in the factor VIII gene identified by
 RT analysis of amplified hemophilia DNA sequences.";

RL Nucleic Acids Res. 15:9797-9805(1987).
 RN [16]
 RP VARIANT HEMA GLN-2228.
 RX MEDLINE=88191889; PubMed=2833855;
 RA Youssoufian H., Antonarakis S.E., Bell W., Griffin A.M.,
 RA Kazazian H.H. Jr.;
 RT "Nonsense and missense mutations in hemophilia A: estimate of the
 RT relative mutation rate at CG dinucleotides.";
 RL Am. J. Hum. Genet. 42:718-725(1988).
 RN [17]
 RP VARIANT HEMA GLY-291.
 RX MEDLINE=88220354; PubMed=2835904;
 RA Youssoufian H., Wong C., Aronis S., Plakoukakis H., Kazazian H.H. Jr.,
 RA Antonarakis S.E.;
 RT "Moderately severe hemophilia A resulting from Glu-->Gly substitution
 RT in exon 7 of the factor VIII gene.";
 RL Am. J. Hum. Genet. 42:867-871(1988).
 RN [18]
 RP VARIANT HEMA CYS-1708.
 RX MEDLINE=89274393; PubMed=2499363;
 RA O'Brien D.P., Tuddenham E.G.;
 RT "Purification and characterization of factor VIII 1,689-Cys: a
 RT nonfunctional cofactor occurring in a patient with severe hemophilia
 RT A.";
 RL Blood 73:2117-2122(1989).
 RN [19]
 RP VARIANT HEMA CYS-391.
 RX MEDLINE=90001543; PubMed=2506948;
 RA Shima M., Ware J., Yoshitaka A., Fukui H., Fulcher C.A.;
 RT "An arginine to cysteine amino acid substitution at a critical
 RT chrombin cleavage site in a dysfunctional factor VIII molecule.";
 RL Blood 74:1612-1617(1989).
 RN [20]
 RP VARIANT HEMA LEU-189.
 RX MEDLINE=90057680; PubMed=2510835;
 RA Chan V., Chan T.K., Tong T.M., Todd D.;
 RT "A novel missense mutation in exon 4 of the factor VIII:C gene
 RT resulting in moderately severe hemophilia A.";
 RL Blood 74:2688-2691(1989).
 RN [21]
 RP VARIANT HEMA LEU-2326.
 RX MEDLINE=89197216; PubMed=2495245;
 RA Inaba H., Fujimaki M., Kazazian H.H. Jr., Antonarakis S.E.;
 RT "Mild hemophilia A resulting from Arg-co-Leu substitution in exon 26
 RT of the factor VIII gene.";
 RL Hum. Genet. 81:335-338(1989).
 RN [22]
 RP VARIANT HEMA HIS-391.
 RX MEDLINE=89264602; PubMed=2498882;
 RA Arii M., Inaba H., Higuchi M., Antonarakis S.E., Kazazian H.H. Jr.,
 RA Fujimaki M., Hoyer L.W.;
 RT "Direct characterization of factor VIII in plasma: detection of a
 RT mutation altering a chrombin cleavage site (arginine-
 RT 372->histidine).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4277-4281(1989).
 RN [23]
 RP VARIANT HEMA CYS-1708.
 RX MEDLINE=90105723; PubMed=2104766;
 RA Arii M., Higuchi M., Antonarakis S.E., Kazazian H.H. Jr.,
 RA Phillips J.A. III, Janco R.L., Hoyer L.W.;
 RT "Characterization of a chrombin cleavage site mutation (Arg 1689 to
 RT Cys) in the factor VIII gene of two unrelated patients with cross-
 RT reacting maternal-positive hemophilia A.";
 RL Blood 75:384-389(1990).
 RN [24]
 RP VARIANTS HEMA GLN-2228 AND LEU-2326.
 RX MEDLINE=90123183; PubMed=2105106;
 RA Casula L., Murru S., Pecorara M., Ristaldi M.S., Restagno G.,
 RA Mancuso G., Morfini M., de Biasi R., Bando F., Carbonara A.;
 RT "Recurrent mutations and three novel rearrangements in the factor VIII
 RT gene of hemophilia A patients of Italian descent.";
 RL Blood 75:662-670(1990).
 RN [25]

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OM protein - protein search, using sw model

Run on: November 25, 2005, 22:42:11 ; Search time 52 Seconds

(Without alignments)
2286.301 Million cell updates/sec

Title: US-10-511-559-73

Perfect score: 7693
Sequence: 1 ATRRYLGNALNELSMDVQSD.....WVHQLRMELVLCGEAQLDY 1438

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep: *
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3: /cgn2_6/ptodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/PCtus_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7693	100.0	1457	2	US-09-001-039B-47
2	7684	99.9	1438	2	US-09-209-916-1
3	7667	99.7	1471	1	US-08-683-839B-3
4	7597	98.8	1447	2	US-09-407-605-4
5	7587	98.6	1445	2	US-09-407-605-3
6	7443	96.8	1461	1	US-08-882-083-2
7	7443	96.8	1661	1	US-08-558-107-2
8	7443	96.8	1661	2	US-09-243-539-2
9	7236	94.1	2332	2	US-10-360-101-329
10	7236	94.1	2351	1	US-08-366-851A-2
11	7236	94.1	2351	2	US-10-133-907-4
12	7236	94.1	2351	2	US-09-001-039B-45
13	7233	94.0	2332	1	US-08-276-594A-2
14	7230	94.0	2351	6	5171844-2
15	7227	93.9	2332	1	US-07-864-004B-4
16	7227	93.9	2332	1	US-08-251-937A-4
17	7227	93.9	2332	1	US-08-212-133A-2
18	7227	93.9	2332	1	US-08-474-503-2
19	7227	93.9	2332	1	US-08-670-707A-2
20	7227	93.9	2332	2	US-09-037-601-2
21	7227	93.9	2332	2	US-09-315-179-2
22	7227	93.9	2332	2	US-09-523-656-2
23	7227	93.9	2332	2	US-09-957-641A-2
24	7227	93.9	2332	4	PCT-US93-03275-4
25	7227	93.9	2351	4	PCT-US94-13200-2
26	7227	93.9	2351	1	US-08-121-202-2
27	7218	93.8	2351	6	5422260-1

28	7188	93.4	2332	2	US-09-324-867-3	Sequence 3, Appl
29	6569	85.4	1467	2	US-09-523-656-38	Sequence 38, Appl
30	6498	84.5	1443	1	US-08-670-707A-39	Sequence 39, Appl
31	6498	84.5	1443	2	US-09-037-601-39	Sequence 39, Appl
32	6498	84.5	1443	2	US-09-315-179-39	Sequence 39, Appl
33	6281	81.6	2343	2	US-09-324-867-2	Sequence 2, Appl
34	6236	81.1	2133	1	US-08-670-707A-37	Sequence 37, Appl
35	6236	81.1	2133	2	US-09-037-601-37	Sequence 37, Appl
36	6236	81.1	2133	2	US-09-315-179-37	Sequence 37, Appl
37	6236	81.1	2133	2	US-09-523-656-30	Sequence 30, Appl
38	6201	80.6	2319	1	US-08-212-133A-8	Sequence 8, Appl
39	6201	80.6	2319	1	US-08-474-503-6	Sequence 6, Appl
40	6201	80.6	2319	1	US-08-670-707A-6	Sequence 6, Appl
41	6201	80.6	2319	2	US-09-037-601-6	Sequence 6, Appl
42	6201	80.6	2319	2	US-09-315-179-6	Sequence 6, Appl
43	6201	80.6	2319	2	US-09-523-656-28	Sequence 28, Appl
44	6201	80.6	2319	4	PCT-US94-13200-6	Sequence 6, Appl
45	6196.5	80.5	2115	2	US-09-324-867-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-001-039B-47
Sequence 47, Application US/09001039B
Patent No. 6818439
GENERAL INFORMATION:
APPLICANT: Jolly, Douglas J.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Respress, James G.
APPLICANT: Depolo, Nicholas J.
APPLICANT: Hsu, David Chi-Tang
APPLICANT: Ibanez, Carlos E.
APPLICANT: Greengard, Judith
APPLICANT: Lee, Will
TITLE OF INVENTION: METHODS FOR ADMINISTRATION OF
TITLE OF INVENTION: RECOMBINANT DELIVERY VEHICLES
TITLE OF INVENTION: OF HEMOPHILIA AND OTHER DISORDERS
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/001.039B
FILING DATE: 13-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McWaters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 1155.005 / 930049.44104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 623-4800
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 1457 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-001-039B-47
Query Match 100.0%; Score 7693; DB 2; Length 1457;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20 ATRRYVLCAGVELSMDYMSDGLGELPVDARPPRVKSPFNTSVYKKTLFVEFTDHLFN 79
QY 61 IAKRPPMGMGLGPTIOAEVYDTVITLKNMASHPVSLHAAGVSYWKASBGAEDDQTSQ 120
Db 80 IAKRPPMGMGLGPTIOAEVYDTVITLKNMASHPVSLHAAGVSYWKASBGAEDDQTSQ 139
QY 121 REKEDDVFPFGSGHTTYWQVLKENGPMASDPLCTYSYLSHVLDVKDLSGLIGALLVCR 180
Db 140 REKEDDVFPFGSGHTTYWQVLKENGPMASDPLCTYSYLSHVLDVKDLSGLIGALLVCR 199
QY 181 EGSIAKETOTLHKFILLFAVPDEGKSMHSETKNSLMODRDAASARAMPKMHNTVNGVYNR 240
Db 200 EGSIAKETOTLHKFILLFAVPDEGKSMHSETKNSLMODRDAASARAMPKMHNTVNGVYNR 259
QY 241 SLPLGIGCHRSKSVYWHVIGMGTTPREVHSIFLEGHTFLVRNHRQASLEISPTFLTAOTLL 300
Db 260 SLPLGIGCHRSKSVYWHVIGMGTTPREVHSIFLEGHTFLVRNHRQASLEISPTFLTAOTLL 319
QY 301 MDLGOFLFLFCHISSHODGMEAYVYKDSCEPEPOLRMKNNEAEDYDDDLTDEMDVYRF 360
Db 320 MDLGOFLFLFCHISSHODGMEAYVYKDSCEPEPOLRMKNNEAEDYDDDLTDEMDVYRF 379
QY 361 DDDNSPSFIQIRSAVAKKPKTWVHNTAAEEDMDYAPLVLPADBSYKSYQLNNGPQRIQ 420
Db 380 DDDNSPSFIQIRSAVAKKPKTWVHNTAAEEDMDYAPLVLPADBSYKSYQLNNGPQRIQ 439
QY 421 RKYKRVKRMATYDTEFTKREAIQHSGLIGPLLYGEVDTLLIFKQNASRPNIYHPGI 480
Db 440 RKYKRVKRMATYDTEFTKREAIQHSGLIGPLLYGEVDTLLIFKQNASRPNIYHPGI 499
QY 481 TDVAPLYSRRLPKGVKHLKDEPILPGEI FKXKWTYVEDGPTKSDPRCLTRYSSFYVME 540
Db 500 TDVAPLYSRRLPKGVKHLKDEPILPGEI FKXKWTYVEDGPTKSDPRCLTRYSSFYVME 559
QY 541 RDLASGLIGPLILCYKESVDQGNQIMDKXNVILFSYFDENRSMYLTENIQRLPNPAG 600
Db 560 RDLASGLIGPLILCYKESVDQGNQIMDKXNVILFSYFDENRSMYLTENIQRLPNPAG 619
QY 601 VQLEDPERQASINMHSINGYVFDLSQSVCLHEVAWYVILSIGQOTDLSVFFSGYTPKH 660
Db 620 VQLEDPERQASINMHSINGYVFDLSQSVCLHEVAWYVILSIGQOTDLSVFFSGYTPKH 679
QY 661 KMVYEDTLTLFPFSGETVFMSEMENGWLILGCHNSDFRNQMTALLKVSQCDKXGTYE 720
Db 680 KMVYEDTLTLFPFSGETVFMSEMENGWLILGCHNSDFRNQMTALLKVSQCDKXGTYE 739
QY 721 DSYEDISAYLISKNNALIEPRSPSONPVLKXHQREITTTIQSOQEEIDYDQDTSIVEMKK 780
Db 740 DSYEDISAYLISKNNALIEPRSPSONPVLKXHQREITTTIQSOQEEIDYDQDTSIVEMKK 799
QY 781 EDFOIYDDEDEKSPRSFOKTRHYFIAVERLMDYGMSSPHVLRNRAQSSGVQFKKV 840
Db 800 EDFOIYDDEDEKSPRSFOKTRHYFIAVERLMDYGMSSPHVLRNRAQSSGVQFKKV 859
QY 841 FOEFTDGSFTQPLVYRGELNEHLGILGPYIRAEVEDNIWTFRNQASRPYSYSSLISYEE 900
Db 860 FOEFTDGSFTQPLVYRGELNEHLGILGPYIRAEVEDNIWTFRNQASRPYSYSSLISYEE 919
QY 901 DORGAERKRVFVNEKTYFKYVQHHMARTKDBFCOKAMAYFSDVDLEOVHSGILGP 960
Db 920 DORGAERKRVFVNEKTYFKYVQHHMARTKDBFCOKAMAYFSDVDLEOVHSGILGP 979
QY 961 LLVCHTINTLPAHSGOVTVQEFALFPTIFDETYSYFENNERCRAPCNIMQMDPTPKE 1020
Db 980 LLVCHTINTLPAHSGOVTVQEFALFPTIFDETYSYFENNERCRAPCNIMQMDPTPKE 1039
QY 1021 NYRFAINGYIMDTLPGLVMAQDQIRWYLLSMGSNENIHSHPSGHVFTVRKKEEYKMA 1080
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Db 1040 NYRFAINGYIMDTLPGLVMAQDQIRWYLLSMGSNENIHSHPSGHVFTVRKKEEYKMA 1099
QY 1081 LYNLYPGVFETVENLBSKAGIMRYECLIGETHLAGMSTLFLVYSNKKOTPLGMAHGIRD 1140
Db 1100 LYNLYPGVFETVENLBSKAGIMRYECLIGETHLAGMSTLFLVYSNKKOTPLGMAHGIRD 1159
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Db 1160 FOITASGOYGOMAKRLRLHYSGSINAMSTKEPSWIKVDLAPMIITHGITQOAROKFS 1219
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Db 1280 HYSIRSLRMEIMCCDINSKSMPLGMSKASISDAQITASSYFTMTKATMSKARLHQ 1339
QY 1321 RSNAMRPOVNNPKEMLOVDFOKTMKVYGTQGVKSLTSMYVKEFLISSQDGHQWTLF 1380
Db 1340 RSNAMRPOVNNPKEMLOVDFOKTMKVYGTQGVKSLTSMYVKEFLISSQDGHQWTLF 1399
QY 1381 FONGKRVFOGNQDSTFPVYNSLDPPLTRYLRIRHPSWVHQIALRMEVIGCEAODLY 1438
Db 1400 FONGKRVFOGNQDSTFPVYNSLDPPLTRYLRIRHPSWVHQIALRMEVIGCEAODLY 1457
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RESULT 2
US-09-209-916-1
; Sequence 1, Application US/09209916
; Patent No. 6358703
; GENERAL INFORMATION:
; APPLICANT: Cho, Myung-Sam
; APPLICANT: Chan, Sham-tuen
; APPLICANT: Kelsey, William
; APPLICANT: Yee, Helena
; TITLE OF INVENTION: Expression System for Factor VIII
; FILE REFERENCE: MSB-7255
; CURRENT APPLICATION NUMBER: US/09/209, 916
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1438
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Derived from
; US-09-209-916-1
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Query Match 99.9%; Score 7684; DB 2; Length 1438;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1437; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATRRYVLCAGVELSMDYMSDGLGELPVDARPPRVKSPFNTSVYKKTLFVEFTDHLFN 60
Db 1 ATRRYVLCAGVELSMDYMSDGLGELPVDARPPRVKSPFNTSVYKKTLFVEFTDHLFN 60
QY 61 IAKRPPMGMGLGPTIOAEVYDTVITLKNMASHPVSLHAAGVSYWKASBGAEDDQTSQ 120
Db 61 IAKRPPMGMGLGPTIOAEVYDTVITLKNMASHPVSLHAAGVSYWKASBGAEDDQTSQ 120
QY 121 REKEDDVFPFGSGHTTYWQVLKENGPMASDPLCTYSYLSHVLDVKDLSGLIGALLVCR 180
Db 121 REKEDDVFPFGSGHTTYWQVLKENGPMASDPLCTYSYLSHVLDVKDLSGLIGALLVCR 180
QY 181 EGSIAKETOTLHKFILLFAVPDEGKSMHSETKNSLMODRDAASARAMPKMHNTVNGVYNR 240
Db 181 EGSIAKETOTLHKFILLFAVPDEGKSMHSETKNSLMODRDAASARAMPKMHNTVNGVYNR 240
QY 241 SLPLGIGCHRSKSVYWHVIGMGTTPREVHSIFLEGHTFLVRNHRQASLEISPTFLTAOTLL 300
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Db 301 MDLQGLFCHISSHQHDGMEAYVKVDCPEEPQLRMKNNEABEDYDDDLTDSMDVVR 360
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Db 361 DDNSPSFIOIRSAVAKKPKTWVHYIAAEBEDMDAPLVLA PDDRSYKSQYLNNGPORIG 420
Qy 421 RYKVKRPMAYTDEFTKTRREALIOHESGILGPLLYGEVDTLLIIFKQASRPYNIYPHGI 480
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Qy 481 TDVAPLSRRLPKGVKHLKDFPILPGELFKYKMTVTVEDGPTKSDPRLCTRYYSFNME 540
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Db 541 RDLASGLIGPLLI CYKESVDORGNQIMSDKRNVLFSVFEDNRSWYLTENIORFLPNPAG 600
Qy 601 VQLEDPPEFOASNIHMSINGVYFDSLOLSVCLHEVAWYIISIGAQTDFLSVFSGYTFKH 660
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Qy 661 KMVYEDTLTLPFSGEYTFMSEMENGMLILGCHNSDFRNQMTALLKVS CDKXTGDYYE 720
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Qy 1261 HYSIRSTLRBMLGCDLNSGMPJGMEKASDAQITASSYFTMPTWSPSKARLHOG 1320
Db 1261 HYSIRSTLRBMLGCDLNSGMPJGMEKASDAQITASSYFTMPTWSPSKARLHOG 1320
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Db 1381 FONGKVVQFQGNODSFTPVVNSLDPLLTRYLRIHPQSWHQAIRNEVLCGEAODLY 1438

RESULT 2
US-10-047-257-1
; Sequence 1, Application US/10047257
; Publication No. US20020115152A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Myung-Sam
; APPLICANT: Chen, Sham-Yuen
; APPLICANT: Kelsey, William
; APPLICANT: Yee, Helena
; TITLE OF INVENTION: Expression System for Factor VIII
; FILE REFERENCE: MSB-7255.2
; CURRENT APPLICATION NUMBER: US/10/047,257
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 1438
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Derived from
US-10-047-257-1

Query Match 99.9%; Score 7684; DB 4; Length 1438;
Best Local Similarity 99.9%; Pred. NO. 0;
Matches 1437; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATRRRYVGAELSDVYQSDLGELPVDARPPRPVPSFPNTSVYVKKTLFVEFTDHLFN 60
Db 1 ATRRRYVGAELSDVYQSDLGELPVDARPPRPVPSFPNTSVYVKKTLFVEFTDHLFN 60
Qy 61 IAKRPPWMLGELPTIOAEVYDYVTITLKNASHPVSLAIVGVSYKASBGAEDDQTSQ 120
Db 61 IAKRPPWMLGELPTIOAEVYDYVTITLKNASHPVSLAIVGVSYKASBGAEDDQTSQ 120
Qy 121 REKEDDVFPFGSGSTYVYQVLKENGPMASDPLCTYVYLHVDTVKRLNSGLIGALLVCR 180
Db 121 REKEDDVFPFGSGSTYVYQVLKENGPMASDPLCTYVYLHVDTVKRLNSGLIGALLVCR 180
Qy 181 EGSIAKEKOTLILKFIILFAVFDGKSMHSETKNSLMQDRDAASARAMPKMTVNGVYNR 240
Db 181 EGSIAKEKOTLILKFIILFAVFDGKSMHSETKNSLMQDRDAASARAMPKMTVNGVYNR 240
Qy 241 SLPLGICHRKSYVWHVIGKTTPEVHSIFLEGHTEFLVRNHRQASLEISPTITLTAOTLL 300
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Db 301 MDLQGLFCHISSHQHDGMEAYVKVDCPEEPQLRMKNNEABEDYDDDLTDSMDVVR 360
Qy 361 DDNSPSFIOIRSAVAKKPKTWVHYIAAEBEDMDAPLVLA PDDRSYKSQYLNNGPORIG 420
Db 361 DDNSPSFIOIRSAVAKKPKTWVHYIAAEBEDMDAPLVLA PDDRSYKSQYLNNGPORIG 420
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Db 421 RYKVKRPMAYTDEFTKTRREALIOHESGILGPLLYGEVDTLLIIFKQASRPYNIYPHGI 480
Qy 481 TDVAPLSRRLPKGVKHLKDFPILPGELFKYKMTVTVEDGPTKSDPRLCTRYYSFNME 540
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Qy 601 VQLEDPPEFOASNIHMSINGVYFDSLOLSVCLHEVAWYIISIGAQTDFLSVFSGYTFKH 660
Db 601 VQLEDPPEFOASNIHMSINGVYFDSLOLSVCLHEVAWYIISIGAQTDFLSVFSGYTFKH 660

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2005, 22:47:56 ; Search time 10 Seconds

(without alignments)
435.854 Million cell updates/sec

Title: US-10-511-559-73

Perfect score: 7693

Sequence: 1 ATRRYVIGAVELSDVMQSD.....WVHQLMRVLCGEADLY 1438

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- 1: Published Applications AA New:
- 2: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	7693	100.0	1438	US-10-511-559-73
2	6569	85.4	1467	US-10-507-956-1
3	1751.5	22.8	1160	US-10-131-826A-234
4	261	3.4	756	US-10-131-826A-392
5	217	2.8	734	US-10-652-893-2
6	217	2.8	734	US-11-137-465-65
7	109	1.4	1614	US-10-821-234-903
8	104.5	1.4	1145	US-10-793-626-1432
9	104	1.4	20	US-10-511-559-84
10	103	1.3	794	US-10-485-517-355
11	98.5	1.3	501	US-10-793-626-244
12	98	1.3	443	US-10-793-626-1860
13	96.5	1.3	1070	US-11/062
14	96.5	1.3	1095	US-11/062
15	96	1.2	1344	US-11-091-643-20
16	95	1.2	760	US-10-821-234-1141
17	95	1.2	989	US-10-793-626-2594
18	94.5	1.2	873	US-10-793-626-3036
19	91.5	1.2	477	US-10-793-626-3250
20	91	1.2	518	US-10-793-626-506
21	91	1.2	835	US-10-501-039-4
22	90	1.2	522	US-10-793-626-604
23	90	1.2	732	US-10-518-599-22
24	89.5	1.2	752	US-10-793-626-348
25	89.5	1.2	1006	US-10-793-626-154

26	89	1.2	619	1	US-10-821-234-1150	Sequence 1150, Ap
27	88.5	1.2	1452	1	US-10-821-234-1102	Sequence 1102, Ap
28	88.5	1.2	4384	1	US-10-821-234-1120	Sequence 1120, Ap
29	87.5	1.1	1237	1	US-10-793-626-96	Sequence 96, Ap
30	87	1.1	628	7	US-11-074-176-244	Sequence 244, Ap
31	86.5	1.1	687	7	US-11-074-176-260	Sequence 260, Ap
32	86.5	1.1	803	1	US-10-821-234-1643	Sequence 1643, Ap
33	86	1.1	15	1	US-10-511-559-81	Sequence 81, Ap
34	86	1.1	15	1	US-10-511-559-1144	Sequence 1144, Ap
35	85.5	1.1	358	1	US-10-821-234-1563	Sequence 1563, Ap
36	85.5	1.1	471	7	US-11-061-869-20	Sequence 20, Ap
37	85.5	1.1	618	1	US-10-793-626-860	Sequence 860, Ap
38	85	1.1	15	1	US-10-511-559-77	Sequence 77, Ap
39	85	1.1	1841	7	US-11-057-058-63	Sequence 63, Ap
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42	84	1.1	619	1	US-10-485-517-374	Sequence 374, Ap
43	84	1.1	919	1	US-10-821-234-951	Sequence 951, Ap
44	83.5	1.1	455	1	US-10-793-626-718	Sequence 718, Ap
45	83.5	1.1	932	7	US-11-017-550-65	Sequence 65, Ap

ALIGNMENTS

RESULT 1
US-10-511-559-73
Sequence 73, Application US/10511559
Publication No. US20050256304A1
GENERAL INFORMATION:
APPLICANT: JONES, Tim
APPLICANT: BAKER, Matthew
TITLE OR INVENTION: MODIFIED FACTOR VIII
FILE REFERENCE: MER-133
CURRENT FILING DATE: US/10/511, 559
PRIORITY FILING DATE: 2004-10-15
PRIORITY APPLICATION NUMBER: PCT/EP03/04063
PRIORITY FILING DATE: 2003-04-17
PRIORITY APPLICATION NUMBER: EP 02008712.8
PRIORITY FILING DATE: 2002-04-18
PRIORITY APPLICATION NUMBER: EP 0306554.4
NUMBER OF SEQ ID NOS: 1147
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 73
LENGTH: 1438
TYPE: PRT
ORGANISM: homo sapiens
US-10-511-559-73

Query Match 100.0%; Score 7693; DB 1; Length 1438;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1438; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	ATRRYYVIGAVELSDVMQSDGLPVDARPPPRVKSFPFTSVYKKTFLVEFTDHLFN	60
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QY	121	REKDDVFPFGSGITTYWQVLKENGPMASDPLCTYVSLSHVDLVKDLNSGLIGALLVCR	180
DB	121	REKDDVFPFGSGITTYWQVLKENGPMASDPLCTYVSLSHVDLVKDLNSGLIGALLVCR	180
QY	181	EGSLAKETOTLHFFILFAVFDGKSMHSTKSLNQDDBAASARAMPKXHTVNGVYNR	240
DB	181	EGSLAKETOTLHFFILFAVFDGKSMHSTKSLNQDDBAASARAMPKXHTVNGVYNR	240
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DB	241	SLPGLICHRKSVYWHVIGMGTTPVHSIFLEGHTFLVRNHRQSLSPITFTLAQTLL	300

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US-10-507-956-1
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; Publication No. US20050256038A1
; GENERAL INFORMATION:
; APPLICANT: Societe de Conseils de Recherches et d Applications Scientifiques
; APPLICANT: (S.C.R.A.S.)
; TITLE OF INVENTION: Stable pharmaceutical composition containing factor VIII
; FILE REFERENCE: 44284.WO01/UMD
; CURRENT APPLICATION NUMBER: US/10/507,956
; PRIOR FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: GB 0207092.8
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1467
; TYPE: PRT
; ORGANISM: Porcine
US-10-507-956-1
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20 AIRRYVGAVELSDMYQSELELRELVDTFRPATAPALPLGSEVLTKTVFVETQLF 79
60 NIAKRPWMGLGPTTQAEVYDTVTTLKXMAHPVSLHAGVSVYKASEGAEYDDQTS 119
80 SVARPRPMGLGPTTQAEVYDTVTTLKXMAHPVSLHAGVSVYKASEGAEYDDQTS 139
120 QREKEDKVPFGSGHYTVQVLYKENGPMASDPLCTYSYSHVDLVNDLSGLIGALLVC 179
140 QREKEDKVPFGSQTYVQVLYKENGPTASDPLCTYSYSHVDLVNDLSGLIGALLVC 199
180 REGSLAKEKTQTHKFFLFAVFDGSKMHSSETKNSLMODRDAASARAMPMTVNGVYN 239
200 REGSLTBERQNLHEFVLPAVFDGSKMHSARNDSTTRAMDAPAPAOAMHTVNGVYN 259
240 RSLPGLIGCHRSKSVYVHVIQMGTTPEVHSI FLEGHTFLVNRHQASLEISPTFLTAQTL 299
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360 FDDNSPSFIQIRSVAKKHPTWVHYIAAEEDMDYAPLVLPDDRYSKQYLANNGPQIRG 419
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420 GRKVKVRMAATDEFTKTRREALIQHSSGILGPLLYGEVDTLLIFKNOASRPYNIYPHGI 479
439 GRKVKVRMAATDEFTKTRREALIQHSSGILGPLLYGEVDTLLIFKNOASRPYNIYPHGI 498
480 ITDVRLPYRRRLPKGVKHLKDPILBGEI FKXKWTYVDEGPTKSDPRCLTRYSSPVNME 539
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540 ERDLASGLIGPLLI CYKESVDQKQIMSDKRNVLFSVFEDNRSWYLTENIQRFLEPNAG 599
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600 GVOLEDPPEQASINMHSINGVYFDSQLQSVCLHEVAWYILSIGAQTDFLSVFFSGYTFKH 659

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OM protein - protein search, using sw model

Run on: November 25, 2005, 23:18:02 ; Search time 1.13793 Seconds
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Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications_AA_New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
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2	75	100.0	1438 1 US-10-511-559-73	Sequence 73, Appl
3	65	86.7	13 1 US-10-511-559-831	Sequence 831, App
4	64	85.3	13 1 US-10-511-559-832	Sequence 832, App
5	58	77.3	13 1 US-10-511-559-833	Sequence 833, App
6	56	74.7	13 1 US-10-511-559-830	Sequence 830, App
7	56	74.7	1467 1 US-10-507-956-1	Sequence 1, Appl
8	51	68.0	13 1 US-10-511-559-834	Sequence 834, App
9	45	60.0	13 1 US-10-511-559-829	Sequence 829, App
10	40	59.3	13 1 US-10-511-559-828	Sequence 828, App
11	37	49.3	534 1 US-10-821-234-1341	Sequence 1341, Ap
12	36	48.0	13 1 US-10-511-559-827	Sequence 827, App
13	34	45.3	409 1 US-10-821-234-892	Sequence 892, App
14	34	45.3	500 1 US-10-821-234-1458	Sequence 1458, Ap
15	33	44.0	826 1 US-10-821-234-1048	Sequence 1048, Ap
16	32	42.7	13 1 US-10-511-559-826	Sequence 826, App
17	32	42.7	119 1 US-10-793-626-1372	Sequence 1372, Ap
18	32	42.7	240 1 US-10-689-742-210	Sequence 210, App
19	32	42.7	314 1 US-10-995-793-74	Sequence 74, Appl
20	32	42.7	555 1 US-10-131-826A-72	Sequence 72, Appl
21	32	42.7	805 1 US-10-518-559-2	Sequence 2, Appl
22	31	41.3	284 1 US-10-510-386-72	Sequence 72, Appl
23	31	41.3	289 1 US-10-793-626-3254	Sequence 3254, Ap
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27	31	41.3	616 1 US-10-131-826A-206	Sequence 206, App
28	31	41.3	709 1 US-11-074-176-158	Sequence 158, App
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61	28	37.3	328 1 US-10-131-826A-34	Sequence 34, Appl
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133	26	34.7	277	1	US-10-667-295-97	Sequence 97, Appl	206	25	33.3	339	7	US-11-010-874-6	Sequence 6, Appl1
134	26	34.7	282	1	US-10-972-587-28	Sequence 28, Appl	207	25	33.3	340	7	US-10-067-974-8	Sequence 8, Appl1
135	26	34.7	288	1	US-10-821-234-1617	Sequence 1617, Ap	208	25	33.3	348	7	US-11-082-389-218	Sequence 218, App
136	26	34.7	296	1	US-10-667-295-96	Sequence 96, Appl	209	25	33.3	354	1	US-10-793-626-3098	Sequence 3098, App
137	26	34.7	327	1	US-10-821-234-1686	Sequence 1686, Ap	210	25	33.3	371	1	US-10-793-626-628	Sequence 628, App
138	26	34.7	333	7	US-11-082-389-202	Sequence 202, App	211	25	33.3	379	1	US-10-131-826A-216	Sequence 216, App
139	26	34.7	339	7	US-11-010-874-5	Sequence 5, Appl1	212	25	33.3	425	1	US-10-793-626-2604	Sequence 2604, App
140	26	34.7	342	7	US-11-152-892-11	Sequence 11, Appl	213	25	33.3	460	1	US-10-821-234-4986	Sequence 986, App
141	26	34.7	358	1	US-10-793-626-918	Sequence 918, App	214	25	33.3	477	1	US-10-131-826A-452	Sequence 452, App
142	26	34.7	361	1	US-10-793-626-160	Sequence 160, App	215	25	33.3	480	7	US-10-131-826A-138	Sequence 138, App
143	26	34.7	399	7	US-11-018-018-3	Sequence 3, Appl1	216	25	33.3	495	1	US-11-074-176-2	Sequence 2, Appl1
144	26	34.7	399	7	US-11-047-757-3	Sequence 3, Appl1	217	25	33.3	523	1	US-10-821-234-1154	Sequence 1154, Ap
145	26	34.7	400	1	US-10-821-234-1534	Sequence 1534, Ap	218	25	33.3	529	1	US-10-131-826A-246	Sequence 246, App
146	26	34.7	406	1	US-10-821-234-1113	Sequence 1113, Ap	219	25	33.3	559	1	US-10-858-720-91	Sequence 91, Appl
147	26	34.7	490	1	US-10-131-826A-356	Sequence 356, App	220	25	33.3	571	1	US-10-821-234-1513	Sequence 1513, Ap
148	26	34.7	516	1	US-10-486-968-52	Sequence 52, Appl	221	25	33.3	596	7	US-10-131-826A-542	Sequence 542, App
149	26	34.7	540	1	US-10-821-234-1456	Sequence 1456, Ap	222	25	33.3	604	1	US-10-793-626-390	Sequence 390, App
150	26	34.7	567	1	US-10-503-051-5	Sequence 5, Appl1	223	25	33.3	614	7	US-11-015-546A-20	Sequence 20, Appl
151	26	34.7	594	1	US-10-131-826A-10	Sequence 10, Appl	224	25	33.3	618	1	US-10-858-720-74	Sequence 74, Appl
152	26	34.7	833	1	US-10-667-295-102	Sequence 102, App	225	25	33.3	633	1	US-10-821-234-1146	Sequence 1146, Ap
153	26	34.7	839	1	US-10-667-295-101	Sequence 101, App	226	25	33.3	644	1	US-10-793-626-1436	Sequence 1436, Ap
154	26	34.7	1094	1	US-10-821-234-1097	Sequence 1097, Ap	227	25	33.3	667	1	US-10-793-626-198	Sequence 198, App
155	26	34.7	1127	1	US-10-821-234-1657	Sequence 1657, Ap	228	25	33.3	687	7	US-11-074-176-280	Sequence 260, App
156	26	34.7	1127	1	US-10-858-730-13	Sequence 13, Appl	229	25	33.3	748	1	US-10-821-234-1479	Sequence 1479, Ap
157	26	34.7	1187	1	US-10-821-234-955	Sequence 955, App	230	25	33.3	756	1	US-10-131-826A-192	Sequence 392, App
158	26	34.7	1196	1	US-10-667-295-100	Sequence 100, App	231	25	33.3	782	1	US-10-972-053-2	Sequence 2, Appl1
159	26	34.7	1255	7	US-11-022-562-213	Sequence 213, App	232	25	33.3	782	1	US-10-972-053-8	Sequence 8, Appl1
160	26	34.7	1338	7	US-10-821-234-1622	Sequence 1622, Ap	233	25	33.3	784	1	US-10-972-053-10	Sequence 10, Appl
161	26	34.7	1338	7	US-11-109-156-23	Sequence 23, Appl	234	25	33.3	792	1	US-10-972-053-12	Sequence 12, Appl
162	26	34.7	2314	7	US-11-013-759-11	Sequence 11, Appl	235	25	33.3	826	1	US-10-793-626-1066	Sequence 1066, Ap
163	26	34.7	2376	7	US-11-096-051-4	Sequence 4, Appl1	236	25	33.3	826	1	US-10-821-234-1202	Sequence 1202, Ap
164	26	34.7	2432	1	US-10-821-234-899	Sequence 899, App	237	25	33.3	1075	1	US-10-821-234-72	Sequence 1209, Ap
165	26	34.7	2516	1	US-10-647-956A-2	Sequence 2, Appl1	238	25	33.3	1189	1	US-10-858-720-102	Sequence 72, App
166	26	34.7	2657	1	US-10-821-234-1262	Sequence 1262, Ap	239	25	33.3	1192	1	US-10-821-234-709	Sequence 72, Appl1
167	26	34.7	2715	7	US-11-096-051-2	Sequence 2, Appl1	240	25	33.3	1992	7	US-11-013-759-3	Sequence 13, Appl1
168	26	34.7	2721	7	US-11-096-051-10	Sequence 10, Appl	241	25	33.3	2047	7	US-11-013-759-4	Sequence 4, Appl1
169	26	34.7	2725	7	US-11-096-051-8	Sequence 8, Appl1	242	25	33.3	2047	7	US-11-013-759-7	Sequence 7, Appl1
170	26	34.7	2919	7	US-10-821-234-1133	Sequence 1133, Ap	243	25	33.3	2053	7	US-11-013-759-9	Sequence 9, Appl1
171	26	34.7	4384	1	US-10-821-234-1120	Sequence 1120, Ap	244	25	33.3				

245	25	33.3	2630	7	US-11-186-731-2	Sequence 2, Appli	318	24	32.0	418	1	US-10-793-626-380	Sequence 380, App
246	25	33.3	7968	7	US-11-186-731-5	Sequence 5, Appli	319	24	32.0	419	1	US-10-821-234-1504	Sequence 1504, Ap
247	24.5	32.7	153	1	US-10-667-295-4	Sequence 4, Appli	320	24	32.0	429	1	US-10-131-826A-94	Sequence 94, Appl
248	24.5	32.7	159	1	US-10-667-295-3	Sequence 3, Appli	321	24	32.0	433	1	US-10-131-826A-334	Sequence 334, App
249	24.5	32.7	174	1	US-10-667-295-2	Sequence 2, Appli	322	24	32.0	434	1	US-10-821-234-1553	Sequence 1553, Ap
250	24.5	32.7	674	1	US-10-821-234-965	Sequence 965, App	323	24	32.0	448	1	US-10-793-626-1740	Sequence 1740, Ap
251	24.5	32.7	1138	1	US-10-509-422-4	Sequence 4, Appli	324	24	32.0	448	7	US-11-013-247A-5	Sequence 5, Appli
252	24.5	32.7	1168	1	US-10-509-422-2	Sequence 2, Appli	325	24	32.0	451	1	US-10-131-826A-126	Sequence 126, App
253	24	32.0	7	7	US-11-064-785-18	Sequence 18, Appli	326	24	32.0	460	1	US-10-858-730-63	Sequence 63, Appl
254	24	32.0	13	1	US-10-511-559-835	Sequence 835, App	327	24	32.0	469	1	US-10-793-626-276	Sequence 276, App
255	24	32.0	52	1	US-10-512-184-40	Sequence 40, Appli	328	24	32.0	485	1	US-10-630-203-4	Sequence 4, Appli
256	24	32.0	53	1	US-10-821-234-1054	Sequence 1054, Ap	329	24	32.0	485	7	US-11-103-037-2	Sequence 2, Appli
257	24	32.0	76	1	US-10-821-234-910	Sequence 910, App	330	24	32.0	501	7	US-11-013-247A-2	Sequence 2, Appli
258	24	32.0	98	7	US-11-053-076-219	Sequence 219, App	331	24	32.0	502	1	US-10-131-826A-548	Sequence 548, App
259	24	32.0	99	7	US-11-053-076-202	Sequence 202, App	332	24	32.0	502	1	US-10-689-742-148	Sequence 148, App
260	24	32.0	111	1	US-10-793-626-730	Sequence 730, App	333	24	32.0	511	1	US-10-131-826A-122	Sequence 122, App
261	24	32.0	111	7	US-11-020-772-17	Sequence 17, Appli	334	24	32.0	529	7	US-11-013-247A-17	Sequence 17, Appli
262	24	32.0	112	7	US-11-020-772-17	Sequence 17, Appli	335	24	32.0	536	1	US-10-131-826A-490	Sequence 490, App
263	24	32.0	134	1	US-10-131-826A-250	Sequence 250, App	336	24	32.0	543	1	US-10-821-234-1158	Sequence 1158, Ap
264	24	32.0	139	7	US-11-013-247A-11	Sequence 11, Appli	337	24	32.0	555	1	US-10-821-234-1015	Sequence 1015, Ap
265	24	32.0	142	1	US-10-986-501-270	Sequence 270, App	338	24	32.0	571	1	US-10-793-626-118	Sequence 118, App
266	24	32.0	144	1	US-10-510-386-154	Sequence 154, App	339	24	32.0	585	1	US-10-821-234-875	Sequence 875, App
267	24	32.0	146	1	US-10-835-615-299	Sequence 299, App	340	24	32.0	596	1	US-10-821-234-1068	Sequence 1068, Ap
268	24	32.0	146	1	US-10-835-615-797	Sequence 797, App	341	24	32.0	604	1	US-10-942-072-4	Sequence 4, Appli
269	24	32.0	159	1	US-10-821-234-1321	Sequence 1321, Ap	342	24	32.0	612	1	US-10-821-234-1101	Sequence 1101, Ap
270	24	32.0	160	7	US-11-010-874-13	Sequence 13, Appli	343	24	32.0	618	1	US-10-821-234-1481	Sequence 1481, Ap
271	24	32.0	160	7	US-11-010-874-14	Sequence 14, Appli	344	24	32.0	634	1	US-10-632-150-26	Sequence 26, Appli
272	24	32.0	169	7	US-10-990-627-3	Sequence 3, Appli	345	24	32.0	635	1	US-10-821-234-927	Sequence 927, App
273	24	32.0	171	1	US-10-793-626-1656	Sequence 1656, Ap	346	24	32.0	637	1	US-10-821-234-961	Sequence 961, App
274	24	32.0	187	1	US-10-980-388-71	Sequence 71, Appli	347	24	32.0	653	1	US-10-131-826A-438	Sequence 25, Appli
275	24	32.0	208	1	US-10-821-234-1118	Sequence 1118, Ap	348	24	32.0	653	7	US-11-135-855-25	Sequence 25, Appli
276	24	32.0	227	1	US-10-977-334-7	Sequence 7, Appli	349	24	32.0	655	1	US-10-793-626-1052	Sequence 1052, Ap
277	24	32.0	230	1	US-10-510-386-198	Sequence 198, App	350	24	32.0	655	1	US-10-793-626-1400	Sequence 1400, App
278	24	32.0	237	1	US-10-884-730-336	Sequence 336, App	351	24	32.0	724	1	US-10-793-626-968	Sequence 968, App
279	24	32.0	242	7	US-11-054-515-1433	Sequence 1433, App	352	24	32.0	734	1	US-10-632-893-2	Sequence 2, Appli
280	24	32.0	250	7	US-11-080-628-23	Sequence 23, Appli	353	24	32.0	747	7	US-11-137-465-65	Sequence 65, Appli
281	24	32.0	258	1	US-10-131-826A-506	Sequence 506, App	354	24	32.0	747	7	US-11-018-018-1	Sequence 1, Appli
282	24	32.0	250	1	US-10-793-626-1686	Sequence 1686, Ap	355	24	32.0	747	7	US-11-047-757-1	Sequence 35, Appli
283	24	32.0	251	7	US-11-054-515-1510	Sequence 1510, Ap	356	24	32.0	763	7	US-11-013-247A-35	Sequence 35, Appli
284	24	32.0	253	1	US-10-633-150-60	Sequence 60, Appli	357	24	32.0	770	1	US-10-821-234-1269	Sequence 1269, Ap
285	24	32.0	256	7	US-11-137-465-34	Sequence 34, Appli	358	24	32.0	773	1	US-10-821-234-1134	Sequence 1134, Ap
286	24	32.0	265	1	US-10-793-626-2748	Sequence 2748, Ap	359	24	32.0	802	1	US-10-510-386-2	Sequence 2, Appli
287	24	32.0	266	1	US-10-884-730-334	Sequence 334, App	360	24	32.0	835	7	US-11-076-187-5	Sequence 5, Appli
288	24	32.0	266	1	US-10-884-730-345	Sequence 345, App	361	24	32.0	835	7	US-11-186-283-2	Sequence 2, Appli
289	24	32.0	275	1	US-10-972-587-18	Sequence 18, Appli	362	24	32.0	867	1	US-10-131-826A-20	Sequence 20, Appli
290	24	32.0	275	7	US-11-065-943-54	Sequence 54, Appli	363	24	32.0	874	1	US-10-510-386-28	Sequence 28, Appli
291	24	32.0	276	1	US-10-972-587-12	Sequence 12, Appli	364	24	32.0	875	1	US-10-858-730-7	Sequence 7, Appli
292	24	32.0	281	1	US-10-131-826A-54	Sequence 54, App	365	24	32.0	888	1	US-10-131-826A-544	Sequence 544, App
293	24	32.0	295	1	US-10-793-626-2946	Sequence 2946, Ap	366	24	32.0	915	1	US-10-647-956A-6	Sequence 6, Appli
294	24	32.0	301	1	US-10-793-626-1396	Sequence 1396, Ap	367	24	32.0	964	7	US-11-016-706-19	Sequence 39, Appli
295	24	32.0	311	1	US-10-131-826A-32	Sequence 32, Appli	368	24	32.0	1032	1	US-10-835-475-1	Sequence 1, Appli
296	24	32.0	311	1	US-10-512-214-16	Sequence 16, Appli	369	24	32.0	1032	7	US-11-014-367-1	Sequence 1, Appli
297	24	32.0	317	1	US-10-512-184-69	Sequence 69, Appli	370	24	32.0	1095	1	US-10-793-626-1514	Sequence 3154, Ap
298	24	32.0	318	1	US-10-793-626-2800	Sequence 2800, Ap	371	24	32.0	1167	1	US-10-942-072-6	Sequence 6, Appli
299	24	32.0	319	1	US-10-131-826A-134	Sequence 134, App	372	24	32.0	1167	1	US-10-942-072-13	Sequence 13, Appli
300	24	32.0	320	1	US-10-512-184-67	Sequence 67, Appli	373	24	32.0	1168	1	US-10-942-072-11	Sequence 11, Appli
301	24	32.0	320	1	US-10-821-234-1627	Sequence 1627, Ap	374	24	32.0	1275	1	US-10-821-234-1598	Sequence 1598, Ap
302	24	32.0	321	1	US-10-793-626-142	Sequence 142, Appli	375	24	32.0	1316	7	US-11-031-643-4	Sequence 4, Appli
303	24	32.0	327	1	US-10-512-184-62	Sequence 62, Appli	376	24	32.0	1410	1	US-10-821-234-1050	Sequence 1050, Ap
304	24	32.0	331	1	US-10-821-234-1650	Sequence 1650, App	377	24	32.0	1432	1	US-10-510-386-218	Sequence 218, App
305	24	32.0	331	1	US-10-793-626-1290	Sequence 1290, Ap	378	24	32.0	1452	1	US-10-821-234-1102	Sequence 1102, Ap
306	24	32.0	339	7	US-11-010-874-3	Sequence 3, Appli	379	24	32.0	1637	1	US-10-821-234-1204	Sequence 1204, Ap
307	24	32.0	347	7	US-11-010-874-4	Sequence 4, Appli	380	24	32.0	1641	1	US-10-986-501-189	Sequence 189, App
308	24	32.0	347	1	US-10-793-626-462	Sequence 462, App	381	23.5	31.3	216	1	US-10-793-626-426	Sequence 426, App
309	24	32.0	347	1	US-10-793-626-1268	Sequence 1268, Ap	382	23.5	31.3	739	1	US-10-131-826A-478	Sequence 478, App
310	24	32.0	350	1	US-10-502-145-1	Sequence 1, Appli	383	23.5	31.3	775	1	US-10-131-826A-120	Sequence 120, App
311	24	32.0	362	7	US-11-013-247A-7	Sequence 7, Appli	384	23.5	31.3	1062	1	US-10-821-234-1079	Sequence 1079, Ap
312	24	32.0	364	7	US-11-013-247A-6	Sequence 6, Appli	385	23.5	31.3	1144	1	US-10-467-962B-89	Sequence 89, Appli
313	24	32.0	387	7	US-11-074-176-232	Sequence 232, App	386	23.5	31.3	1493	7	US-11-004-057-4	Sequence 4, Appli
314	24	32.0	395	7	US-11-074-176-188	Sequence 188, App	387	23.5	31.3	1493	7	US-11-004-057-21	Sequence 21, Appli
315	24	32.0	398	1	US-10-131-826A-348	Sequence 348, App	388	23	30.7	12	1	US-10-997-066-26	Sequence 26, Appli
316	24	32.0	414	1	US-10-821-234-1170	Sequence 1170, Ap	389	23	30.7	17	1	US-10-518-341-14	Sequence 14, Appli
317	24	32.0	415	1	US-10-627-633-2	Sequence 2, Appli	390	23	30.7	19	1	US-10-939-890-251	Sequence 251, App

391	23	30.7	56	1	US-10-997-201A-16	Sequence 16, Appl	464	23	30.7	189	1	US-10-793-626-2692	Sequence 2692, Ap
392	23	30.7	60	1	US-10-502-972-11	Sequence 11, Appl	465	23	30.7	193	1	US-10-981-873-1	Sequence 1, Appl1
393	23	30.7	91	1	US-10-632-150-30	Sequence 30, Appl	466	23	30.7	196	1	US-10-793-626-1088	Sequence 2088, Ap
394	23	30.7	96	1	US-10-689-742-144	Sequence 144, App	467	23	30.7	196	1	US-10-821-234-1682	Sequence 1682, Ap
395	23	30.7	98	1	US-10-614-559-10	Sequence 10, Appl	468	23	30.7	197	1	US-10-632-150-162	Sequence 32, Appl
396	23	30.7	105	7	US-11-053-076-74	Sequence 74, Appl	469	23	30.7	202	1	US-10-793-626-1108	Sequence 1108, Ap
397	23	30.7	111	7	US-11-053-076-63	Sequence 63, Appl	470	23	30.7	203	1	US-10-793-626-1138	Sequence 1138, Ap
398	23	30.7	119	1	US-10-793-626-424	Sequence 424, Ap	471	23	30.7	208	1	US-10-793-626-124	Sequence 124, App
399	23	30.7	121	1	US-10-821-234-1692	Sequence 1692, Ap	472	23	30.7	209	1	US-10-485-517-104	Sequence 404, App
400	23	30.7	124	1	US-10-793-626-1274	Sequence 1274, Ap	473	23	30.7	210	1	US-10-986-501-115	Sequence 115, App
401	23	30.7	145	7	US-11-082-389-310	Sequence 310, App	474	23	30.7	212	1	US-10-793-626-1622	Sequence 1622, Ap
402	23	30.7	146	1	US-10-835-615-264	Sequence 264, App	475	23	30.7	215	1	US-10-793-626-596	Sequence 596, App
403	23	30.7	146	1	US-10-835-615-266	Sequence 266, App	476	23	30.7	215	1	US-10-793-626-2258	Sequence 2258, Ap
404	23	30.7	146	1	US-10-835-615-267	Sequence 267, App	477	23	30.7	217	7	US-11-082-389-54	Sequence 54, Appl
405	23	30.7	146	1	US-10-835-615-269	Sequence 269, App	478	23	30.7	219	1	US-10-793-626-2206	Sequence 2206, Ap
406	23	30.7	146	1	US-10-835-615-274	Sequence 274, App	479	23	30.7	222	1	US-10-821-234-1417	Sequence 1417, Ap
407	23	30.7	146	1	US-10-835-615-279	Sequence 279, App	480	23	30.7	225	1	US-10-131-826A-282	Sequence 282, App
408	23	30.7	146	1	US-10-835-615-280	Sequence 280, App	481	23	30.7	228	1	US-10-793-626-1166	Sequence 1166, Ap
409	23	30.7	146	1	US-10-835-615-286	Sequence 286, App	482	23	30.7	234	1	US-10-821-234-1515	Sequence 1515, Ap
410	23	30.7	146	1	US-10-835-615-289	Sequence 289, App	483	23	30.7	237	1	US-10-793-626-1744	Sequence 1744, Ap
411	23	30.7	146	1	US-10-835-615-292	Sequence 292, App	484	23	30.7	237	7	US-11-082-389-56	Sequence 56, Appl
412	23	30.7	146	1	US-10-835-615-293	Sequence 293, App	485	23	30.7	237	7	US-11-054-515-2111	Sequence 2111, Ap
413	23	30.7	146	1	US-10-835-615-294	Sequence 294, App	486	23	30.7	242	7	US-11-074-176-116	Sequence 116, App
414	23	30.7	146	1	US-10-835-615-302	Sequence 302, App	487	23	30.7	242	7	US-11-179-977-14	Sequence 14, Appl
415	23	30.7	146	1	US-10-835-615-303	Sequence 303, App	488	23	30.7	249	1	US-10-967-527A-21	Sequence 21, Appl
416	23	30.7	146	1	US-10-835-615-309	Sequence 309, App	489	23	30.7	250	7	US-10-742-634-1-11	Sequence 3239, Ap
417	23	30.7	146	1	US-10-835-615-311	Sequence 311, App	490	23	30.7	250	7	US-11-054-515-2239	Sequence 1948, Ap
418	23	30.7	146	1	US-10-835-615-313	Sequence 313, App	491	23	30.7	252	7	US-11-054-515-1992	Sequence 1992, Ap
419	23	30.7	146	1	US-10-835-615-314	Sequence 314, App	492	23	30.7	257	1	US-10-793-626-862	Sequence 862, App
420	23	30.7	146	1	US-10-835-615-316	Sequence 316, App	493	23	30.7	257	1	US-10-793-626-862	Sequence 862, App
421	23	30.7	146	1	US-10-835-615-319	Sequence 319, App	494	23	30.7	257	1	US-10-793-626-862	Sequence 862, App
422	23	30.7	146	1	US-10-835-615-320	Sequence 320, App	495	23	30.7	259	1	US-10-510-366-52	Sequence 52, Appl
423	23	30.7	146	1	US-10-835-615-324	Sequence 324, App	496	23	30.7	260	1	US-10-485-517-154	Sequence 354, App
424	23	30.7	146	1	US-10-835-615-325	Sequence 325, App	497	23	30.7	261	1	US-10-485-517-150	Sequence 150, App
425	23	30.7	146	1	US-10-835-615-327	Sequence 327, App	498	23	30.7	263	1	US-10-131-826A-484	Sequence 484, App
426	23	30.7	146	1	US-10-835-615-328	Sequence 328, App	499	23	30.7	263	1	US-10-821-234-1403	Sequence 1403, Ap
427	23	30.7	146	1	US-10-835-615-329	Sequence 329, App	500	23	30.7	268	1	US-10-821-234-466	Sequence 466, App
428	23	30.7	146	1	US-10-835-615-333	Sequence 333, App	501	23	30.7	269	1	US-10-972-567-16	Sequence 16, Appl
429	23	30.7	146	1	US-10-835-615-335	Sequence 335, App	502	23	30.7	271	1	US-10-793-626-1156	Sequence 1156, Ap
430	23	30.7	146	1	US-10-835-615-336	Sequence 336, App	503	23	30.7	276	7	US-11-091-100-16	Sequence 16, Appl
431	23	30.7	146	1	US-10-835-615-337	Sequence 337, App	504	23	30.7	278	7	US-10-957-569-45	Sequence 45, Appl
432	23	30.7	146	1	US-10-835-615-338	Sequence 338, App	505	23	30.7	286	7	US-11-179-977-9	Sequence 9, Appl1
433	23	30.7	146	1	US-10-835-615-421	Sequence 421, App	506	23	30.7	291	1	US-10-821-234-1560	Sequence 1560, Ap
434	23	30.7	146	1	US-10-835-615-429	Sequence 429, App	507	23	30.7	299	1	US-10-858-720-17	Sequence 17, Appl
435	23	30.7	146	1	US-10-835-615-431	Sequence 431, App	508	23	30.7	309	7	US-11-109-156-24	Sequence 24, Appl
436	23	30.7	146	1	US-10-835-615-434	Sequence 434, App	509	23	30.7	309	7	US-11-109-156-39	Sequence 39, Appl
437	23	30.7	146	1	US-10-835-615-477	Sequence 477, App	510	23	30.7	310	7	US-11-082-389-106	Sequence 306, App
438	23	30.7	146	1	US-10-835-615-577	Sequence 577, App	511	23	30.7	318	1	US-10-793-626-3118	Sequence 3118, Ap
439	23	30.7	146	1	US-10-835-615-578	Sequence 578, App	512	23	30.7	318	1	US-10-821-234-1117	Sequence 1117, Ap
440	23	30.7	146	1	US-10-835-615-579	Sequence 579, App	513	23	30.7	319	7	US-11-074-176-74	Sequence 74, Appl
441	23	30.7	146	1	US-10-835-615-879	Sequence 879, App	514	23	30.7	322	7	US-11-082-389-188	Sequence 188, App
442	23	30.7	146	1	US-10-835-615-981	Sequence 981, App	515	23	30.7	328	1	US-10-821-234-1671	Sequence 1671, Ap
443	23	30.7	146	1	US-10-835-615-911	Sequence 911, App	516	23	30.7	329	1	US-10-485-517-330	Sequence 330, App
444	23	30.7	149	1	US-10-821-234-1244	Sequence 1244, App	517	23	30.7	339	7	US-11-010-874-2	Sequence 2, Appl1
445	23	30.7	150	1	US-10-997-437A-4	Sequence 4, Appl1	518	23	30.7	343	1	US-10-131-826A-162	Sequence 162, App
446	23	30.7	150	1	US-10-793-626-840	Sequence 840, App	519	23	30.7	356	1	US-10-980-388-70	Sequence 70, Appl
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449	23	30.7	160	1	US-10-793-626-2940	Sequence 2940, Ap	522	23	30.7	371	1	US-10-821-234-1010	Sequence 1010, Ap
450	23	30.7	160	7	US-11-010-874-12	Sequence 12, Appl	523	23	30.7	373	1	US-10-131-826A-388	Sequence 388, App
451	23	30.7	162	1	US-10-793-626-614	Sequence 614, App	524	23	30.7	374	7	US-11-051-267-20	Sequence 20, Appl
452	23	30.7	163	1	US-10-793-626-2330	Sequence 2330, Ap	525	23	30.7	376	7	US-11-182-752-2	Sequence 2, Appl1
453	23	30.7	166	1	US-10-821-234-1293	Sequence 1293, Ap	526	23	30.7	377	7	US-11-152-892-8	Sequence 8, Appl1
454	23	30.7	168	7	US-11-010-874-7	Sequence 7, Appl1	527	23	30.7	388	7	US-10-979-821-52	Sequence 52, Appl
455	23	30.7	168	7	US-11-010-874-8	Sequence 8, Appl1	528	23	30.7	389	1	US-10-979-821-2	Sequence 2, Appl1
456	23	30.7	168	7	US-11-010-874-9	Sequence 9, Appl1	529	23	30.7	391	1	US-10-793-626-1336	Sequence 1236, Ap
457	23	30.7	168	7	US-11-010-874-10	Sequence 10, Appl	530	23	30.7	391	1	US-10-821-234-1487	Sequence 1487, Ap
458	23	30.7	168	7	US-11-010-874-11	Sequence 11, Appl	531	23	30.7	399	1	US-10-926-709-17	Sequence 17, Appl
459	23	30.7	182	1	US-10-667-295-63	Sequence 63, Appl	532	23	30.7	407	1	US-10-793-626-1578	Sequence 1578, Ap
460	23	30.7	185	1	US-10-821-234-1384	Sequence 1384, Ap	533	23	30.7	416	1	US-10-793-626-2	Sequence 2, Appl1
461	23	30.7	185	1	US-10-821-234-1498	Sequence 1498, Ap	534	23	30.7	416	7	US-11-016-706-38	Sequence 38, Appl
462	23	30.7	185	1	US-10-967-527A-10	Sequence 10, Appl	535	23	30.7	417	1	US-10-821-234-1365	Sequence 1365, Ap
463	23	30.7	189	1	US-10-793-626-1998	Sequence 1998, Ap	536	23	30.7	417	7	US-11-182-752-4	Sequence 4, Appl1

537	23	30.7	426	1	US-10-131-826A-218	Sequence 218, App	610	22.5	30.0	405	1	US-10-793-626-2752	Sequence 2752, App
538	23	30.7	430	1	US-10-821-234-1437	Sequence 1437, Ap	611	22.5	30.0	425	1	US-10-793-626-1012	Sequence 1012, Ap
539	23	30.7	431	1	US-10-485-517-182	Sequence 182, App	612	22.5	30.0	425	1	US-10-793-626-2434	Sequence 2434, Ap
540	23	30.7	440	7	US-11-082-389-106	Sequence 106, App	613	22.5	30.0	860	7	US-11-022-562-217	Sequence 217, App
541	23	30.7	447	1	US-10-523-588-16	Sequence 16, App	614	22.5	30.0	952	1	US-10-821-224-1557	Sequence 1557, App
542	23	30.7	448	1	US-10-510-386-24	Sequence 24, App	615	22	29.3	19	1	US-10-939-890-245	Sequence 245, App
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546	23	30.7	483	1	US-10-630-203-30	Sequence 30, App	619	22	29.3	72	1	US-10-689-742-118	Sequence 118, App
547	23	30.7	492	1	US-10-821-234-1108	Sequence 1108, Ap	620	22	29.3	95	7	US-11-053-076-181	Sequence 181, App
548	23	30.7	496	1	US-10-793-626-1832	Sequence 1832, Ap	621	22	29.3	104	1	US-10-995-995-1A-21	Sequence 21, App
549	23	30.7	493	1	US-10-793-626-1030	Sequence 1030, Ap	622	22	29.3	104	1	US-10-689-742-106	Sequence 706, App
550	23	30.7	497	1	US-10-821-234-1358	Sequence 1358, Ap	623	22	29.3	106	7	US-11-053-076-112	Sequence 12, App
551	23	30.7	498	1	US-10-510-947-9	Sequence 9, App	624	22	29.3	108	1	US-10-986-501-151	Sequence 151, App
552	23	30.7	502	7	US-11-021-441-7	Sequence 7, App	625	22	29.3	113	1	US-10-793-626-1378	Sequence 1378, Ap
553	23	30.7	503	7	US-11-013-247A-4	Sequence 4, App	626	22	29.3	117	1	US-10-821-224-1362	Sequence 1362, Ap
554	23	30.7	519	1	US-10-821-234-1373	Sequence 1373, Ap	627	22	29.3	120	1	US-10-793-626-2214	Sequence 2214, Ap
555	23	30.7	526	1	US-10-667-295-139	Sequence 139, App	628	22	29.3	120	1	US-10-793-626-2376	Sequence 2376, Ap
556	23	30.7	532	1	US-10-821-234-1071	Sequence 1071, Ap	629	22	29.3	122	1	US-10-821-234-1239	Sequence 1239, Ap
557	23	30.7	534	1	US-10-510-386-230	Sequence 230, App	630	22	29.3	125	1	US-10-927-641-76	Sequence 76, App
558	23	30.7	537	1	US-10-821-234-1427	Sequence 1427, Ap	631	22	29.3	129	1	US-10-501-039-8	Sequence 8, App
559	23	30.7	538	1	US-10-793-626-260	Sequence 260, App	632	22	29.3	134	1	US-10-986-501-114	Sequence 114, App
560	23	30.7	539	1	US-10-793-626-888	Sequence 888, App	633	22	29.3	134	1	US-10-986-501-199	Sequence 199, App
561	23	30.7	546	1	US-10-821-234-902	Sequence 902, App	634	22	29.3	140	1	US-10-793-626-1866	Sequence 1866, App
562	23	30.7	563	7	US-11-021-441-9	Sequence 9, App	635	22	29.3	143	1	US-10-835-615-590	Sequence 590, App
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564	23	30.7	574	1	US-10-518-341-1	Sequence 1, App	637	22	29.3	146	1	US-10-835-615-7	Sequence 7, App
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568	23	30.7	581	7	US-11-021-441-11	Sequence 11, App	641	22	29.3	146	1	US-10-835-615-163	Sequence 163, App
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570	23	30.7	585	7	US-11-012-762-6	Sequence 6, App	643	22	29.3	146	1	US-10-835-615-268	Sequence 268, App
571	23	30.7	619	1	US-10-485-517-374	Sequence 374, App	644	22	29.3	146	1	US-10-835-615-270	Sequence 270, App
572	23	30.7	625	1	US-10-131-826A-70	Sequence 70, App	645	22	29.3	146	1	US-10-835-615-271	Sequence 271, App
573	23	30.7	643	7	US-11-137-465-54	Sequence 54, App	646	22	29.3	146	1	US-10-835-615-272	Sequence 272, App
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576	23	30.7	653	7	US-11-137-465-55	Sequence 55, App	649	22	29.3	146	1	US-10-835-615-276	Sequence 276, App
577	23	30.7	690	1	US-10-131-826A-306	Sequence 306, App	650	22	29.3	146	1	US-10-835-615-277	Sequence 277, App
578	23	30.7	692	7	US-11-038-284-33	Sequence 33, App	651	22	29.3	146	1	US-10-835-615-278	Sequence 278, App
579	23	30.7	711	1	US-10-821-234-1017	Sequence 1017, Ap	652	22	29.3	146	1	US-10-835-615-281	Sequence 281, App
580	23	30.7	754	1	US-10-793-626-1296	Sequence 1296, Ap	653	22	29.3	146	1	US-10-835-615-282	Sequence 282, App
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582	23	30.7	794	1	US-10-485-517-335	Sequence 335, App	655	22	29.3	146	1	US-10-835-615-284	Sequence 284, App
583	23	30.7	812	7	US-11-010-874-1	Sequence 1, App	656	22	29.3	146	1	US-10-835-615-285	Sequence 285, App
584	23	30.7	824	1	US-10-957-569-31	Sequence 31, App	657	22	29.3	146	1	US-10-835-615-287	Sequence 287, App
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588	23	30.7	870	7	US-11-082-389-384	Sequence 384, App	661	22	29.3	146	1	US-10-835-615-295	Sequence 295, App
589	23	30.7	873	7	US-10-793-626-3036	Sequence 3036, Ap	662	22	29.3	146	1	US-10-835-615-296	Sequence 296, App
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592	23	30.7	882	7	US-11-012-762-34	Sequence 34, App	665	22	29.3	146	1	US-10-835-615-300	Sequence 300, App
593	23	30.7	886	7	US-10-821-234-1390	Sequence 1390, Ap	666	22	29.3	146	1	US-10-835-615-301	Sequence 301, App
594	23	30.7	889	7	US-11-038-284-15	Sequence 15, App	667	22	29.3	146	1	US-10-835-615-304	Sequence 304, App
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598	23	30.7	1035	7	US-11-021-441-4	Sequence 4, App	671	22	29.3	146	1	US-10-835-615-308	Sequence 308, App
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600	23	30.7	1125	1	US-10-821-234-1444	Sequence 1444, Ap	673	22	29.3	146	1	US-10-835-615-312	Sequence 312, App
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604	23	30.7	1255	7	US-11-023-562-235	Sequence 235, App	677	22	29.3	146	1	US-10-835-615-321	Sequence 321, App
605	23	30.7	1501	1	US-10-793-626-2850	Sequence 2850, Ap	678	22	29.3	146	1	US-10-835-615-322	Sequence 322, App
606	23	30.7	1502	1	US-10-821-234-916	Sequence 916, App	679	22	29.3	146	1	US-10-835-615-323	Sequence 323, App
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609	22.5	30.0	276	1	US-10-972-587-10	Sequence 10, App	682	22	29.3	146	1	US-10-835-615-331	Sequence 331, App

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684	22	29.3	146	1	US-10-835-615-334	Sequence 334, App	757	22	29.3	146	1	US-10-835-615-413	Sequence 413, App
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689	22	29.3	146	1	US-10-835-615-342	Sequence 342, App	762	22	29.3	146	1	US-10-835-615-418	Sequence 418, App
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695	22	29.3	146	1	US-10-835-615-348	Sequence 348, App	768	22	29.3	146	1	US-10-835-615-425	Sequence 425, App
696	22	29.3	146	1	US-10-835-615-349	Sequence 349, App	769	22	29.3	146	1	US-10-835-615-426	Sequence 426, App
697	22	29.3	146	1	US-10-835-615-350	Sequence 350, App	770	22	29.3	146	1	US-10-835-615-427	Sequence 427, App
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702	22	29.3	146	1	US-10-835-615-355	Sequence 355, App	775	22	29.3	146	1	US-10-835-615-435	Sequence 435, App
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981      22      29.3      146      1      US-10-835-615-801      Sequence 801, App
982      22      29.3      146      1      US-10-835-615-803      Sequence 803, App
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993      22      29.3      146      1      US-10-835-615-825      Sequence 825, App
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995      22      29.3      146      1      US-10-835-615-835      Sequence 835, App
996      22      29.3      146      1      US-10-835-615-837      Sequence 837, App
997      22      29.3      146      1      US-10-835-615-839      Sequence 839, App
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ALIGNMENTS

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; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Epitope of human Factor VIII
US-10-511-559-80

Query Match      100.0%; Score 75; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.3e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1      1      MSSSPHVLNRRAQSG 15

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; Sequence 73, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
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; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 1438
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-511-559-73

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Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1      1      MSSSPHVLNRRAQSG 15
Db      817      817      MSSSPHVLNRRAQSG 831
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; Sequence 831, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 831
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-831

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Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 832, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2005, 23:10:10 ; Search time 29.6897 Seconds
(without alignments)
211.098 Million cell updates/sec

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Perfect score: 75
Sequence: 1 MSSSPHYLRNAQSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	75	100.0	20	US-10-433-273-59	Sequence 59, Appl
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4	75	100.0	1424	US-10-472-516-5	Sequence 5, Appl
5	75	100.0	1424	US-10-968-286-5	Sequence 5, Appl
6	75	100.0	1438	US-10-006-091-1	Sequence 1, Appl
7	75	100.0	1438	US-10-047-257-1	Sequence 1, Appl
8	75	100.0	1438	US-10-225-900-1	Sequence 1, Appl
9	75	100.0	1457	US-10-813-507-13	Sequence 13, Appl
10	75	100.0	1457	US-10-813-507-17	Sequence 17, Appl
11	75	100.0	1459	US-10-239-498A-4	Sequence 4, Appl
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13	75	100.0	1459	US-10-239-498A-15	Sequence 15, Appl
14	75	100.0	1471	US-10-095-718-2	Sequence 2, Appl
15	75	100.0	1471	US-10-681-970-2	Sequence 2, Appl
16	75	100.0	2096	US-10-741-600-1032	Sequence 1032, Ap
17	75	100.0	2332	US-09-957-641-2	Sequence 2, Appl
18	75	100.0	2332	US-10-187-319-2	Sequence 2, Appl
19	75	100.0	2332	US-10-131-510A-2	Sequence 2, Appl
20	75	100.0	2332	US-10-445-235-2	Sequence 2, Appl
21	75	100.0	2332	US-10-360-101-229	Sequence 229, App
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23	75	100.0	2332	US-10-465-998A-1	Sequence 1, Appl
24	75	100.0	2332	US-10-353-733-1	Sequence 1, Appl
25	75	100.0	2332	US-10-721-997A-34	Sequence 34, Appl
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60	56	74.7	2133	US-10-973-941-3	Sequence 3, Appl
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83	39	52.0	131	US-10-289-762-42	Sequence 42, Appl
84	39	52.0	251	US-09-768-826-35	Sequence 35, Appl
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86	39	52.0	251	US-10-874-484-35	Sequence 35, Appl
87	39	52.0	314	US-09-768-826-54	Sequence 54, Appl
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91	39	52.0	405	US-10-450-763-182748	Sequence 182748, A
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108	38	50.7	245	4	US-10-425-115-355320	Sequence 325320,	181	37	49.3	1038	4	US-10-408-765A-843	Sequence 843, App
109	38	50.7	264	4	US-10-425-114-51597	Sequence 51597, A	182	37	49.3	1038	5	US-10-772-626-76	Sequence 76, Appl
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117	38	50.7	598	4	US-10-425-115-187115	Sequence 187115,	190	36.5	48.7	394	4	US-10-282-122A-56667	Sequence 56667, A
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147	37	49.3	143	4	US-10-767-701-60076	Sequence 60076, A	220	36	48.0	551	4	US-10-156-761-14690	Sequence 14690, A
148	37	49.3	144	4	US-10-425-115-278919	Sequence 278919,	221	36	48.0	662	5	US-10-471-758-4	Sequence 4, Appl1
149	37	49.3	189	4	US-10-437-963-169720	Sequence 169720,	222	36	48.0	682	4	US-10-282-122A-50555	Sequence 50595, A
150	37	49.3	232	4	US-10-425-115-275767	Sequence 275767,	223	36	48.0	775	4	US-10-369-493-12761	Sequence 12761, A
151	37	49.3	245	6	US-11-097-143-2358	Sequence 2358, App	224	36	48.0	925	5	US-10-732-923-8664	Sequence 8664, App
152	37	49.3	272	5	US-10-211-028-8	Sequence 8, Appl1	225	36	48.0	1173	4	US-10-369-493-5025	Sequence 5025, A
153	37	49.3	343	4	US-10-425-114-41194	Sequence 41194, A	226	36	48.0	1359	5	US-10-788-746-3	Sequence 3, Appl1
154	37	49.3	353	4	US-10-369-493-7303	Sequence 7303, App	227	36	48.0	1425	5	US-10-450-763-53703	Sequence 53703, A
155	37	49.3	360	4	US-10-437-963-169721	Sequence 169721,	228	36	48.0	1510	6	US-10-1097-143-10140	Sequence 10140, A
156	37	49.3	361	4	US-10-282-122A-78247	Sequence 78247, A	229	35.5	47.3	192	4	US-10-767-701-60707	Sequence 60707, A
157	37	49.3	362	4	US-10-369-493-8480	Sequence 8480, App	230	35.5	47.3	346	4	US-10-437-963-105378	Sequence 105378,
158	37	49.3	366	4	US-10-282-122A-49518	Sequence 49518, A	231	35	46.7	35	4	US-10-425-115-288852	Sequence 288852,
159	37	49.3	368	4	US-10-369-493-4545	Sequence 4545, App	232	35	46.7	56	4	US-10-029-386-23650	Sequence 30267, A
160	37	49.3	369	4	US-10-282-122A-50635	Sequence 50635, A	233	35	46.7	69	4	US-10-424-599-23650	Sequence 236540,
161	37	49.3	371	4	US-10-282-122A-47865	Sequence 47865, A	234	35	46.7	78	4	US-10-425-115-298371	Sequence 298371,
162	37	49.3	375	4	US-10-282-122A-44783	Sequence 44783, A	235	35	46.7	89	4	US-10-424-599-917635	Sequence 176365,
163	37	49.3	406	4	US-10-437-963-124075	Sequence 124075,	236	35	46.7	87	4	US-10-425-115-316622	Sequence 316622,
164	37	49.3	415	4	US-10-424-599-177033	Sequence 177033,	237	35	46.7	90	4	US-10-437-963-128059	Sequence 128059,
165	37	49.3	416	4	US-10-282-122A-47593	Sequence 47593, A	238	35	46.7	90	4	US-10-425-115-288259	Sequence 288259,
166	37	49.3	445	4	US-10-282-122A-47985	Sequence 47985, A	239	35	46.7	101	4	US-10-424-599-292959	Sequence 292959,
167	37	49.3	451	4	US-10-695-243-26	Sequence 26, Appl1	240	35	46.7	117	4	US-10-424-599-263905	Sequence 263905,
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171	37	49.3	514	4	US-10-029-386-32812	Sequence 32912, A	244	35	46.7	130	4	US-10-001-889-93	Sequence 93, Appl1
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173	37	49.3	534	4	US-10-408-765A-1377	Sequence 1377, App	246	35	46.7	148	4	US-10-437-963-192537	Sequence 192537,

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249	35	46.7	180	5	US-10-856-499-834	Sequence 834, App	322	34.5	46.0	705	3	US-09-815-242-5764	Sequence 12463, A
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251	35	46.7	202	4	US-10-264-237-2382	Sequence 2382, App	324	34.5	46.0	819	4	US-10-104-047-7755	Sequence 2755, App
252	35	46.7	208	4	US-10-767-701-51746	Sequence 51746, A	325	34.5	46.0	47	4	US-10-425-115-208554	Sequence 20855, App
253	35	46.7	225	4	US-10-112-944-827	Sequence 827, App	326	34	45.3	48	4	US-10-424-599-157689	Sequence 257689
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268	35	46.7	385	4	US-10-425-115-339141	Sequence 339141, A	341	34	45.3	85	3	US-09-925-302-841	Sequence 841, App
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274	35	46.7	391	4	US-10-369-493-16280	Sequence 16280, A	347	34	45.3	96	4	US-10-160-162-175	Sequence 175, App
275	35	46.7	391	4	US-10-282-122A-46684	Sequence 46684, A	348	34	45.3	96	5	US-10-936-773-175	Sequence 175, App
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278	35	46.7	394	4	US-10-369-493-902	Sequence 902, App	351	34	45.3	100	4	US-10-425-115-185176	Sequence 185176, A
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286	35	46.7	521	4	US-10-094-749-2671	Sequence 2671, App	359	34	45.3	154	5	US-10-450-763-31713	Sequence 31713, A
287	35	46.7	546	4	US-10-437-963-163294	Sequence 163294, A	360	34	45.3	157	4	US-10-424-599-330384	Sequence 330384, A
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289	35	46.7	583	5	US-10-870-690-55	Sequence 55, App	362	34	45.3	163	4	US-10-767-701-39912	Sequence 39912, A
290	35	46.7	583	5	US-10-870-690-61	Sequence 61, App	363	34	45.3	166	3	US-09-925-301-1556	Sequence 1556, App
291	35	46.7	584	5	US-10-381-530-30	Sequence 30, App	364	34	45.3	172	4	US-10-424-599-205867	Sequence 205867, A
292	35	46.7	584	5	US-10-870-690-57	Sequence 57, App	365	34	45.3	175	4	US-10-437-963-163323	Sequence 163323, A
293	35	46.7	584	5	US-10-870-690-59	Sequence 59, App	366	34	45.3	182	4	US-10-437-963-104126	Sequence 104126, A
294	35	46.7	584	5	US-10-870-690-67	Sequence 67, App	367	34	45.3	185	4	US-10-425-115-294025	Sequence 294025, A
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296	35	46.7	585	5	US-10-870-690-65	Sequence 65, App	369	34	45.3	206	4	US-10-425-115-255967	Sequence 255967, A
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299	35	46.7	708	6	US-11-097-143-10932	Sequence 10932, A	372	34	45.3	215	6	US-11-097-143-9435	Sequence 9435, App
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306	35	46.7	1311	4	US-10-369-493-5939	Sequence 5939, App	379	34	45.3	235	4	US-10-153-668-59	Sequence 668, App
307	35	46.7	1363	5	US-10-732-923-3336	Sequence 3336, App	380	34	45.3	237	3	US-09-828-644-72	Sequence 72, App
308	35	46.7	1583	4	US-10-437-963-159486	Sequence 159486, A	381	34	45.3	241	4	US-10-425-114-32143	Sequence 32143, A
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314	35	46.7	1911	4	US-10-115-482-24	Sequence 24, App	387	34	45.3	275	5	US-10-678-639-38	Sequence 38, App
315	34.5	46.0	39	4	US-10-425-115-189768	Sequence 189768, A	388	34	45.3	277	3	US-09-847-102A-73	Sequence 73, App
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319	34.5	46.0	402	3	US-09-815-242-13877	Sequence 13877, A	392	34	45.3	282	3	US-09-815-242-13761	Sequence 13761, A

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394	34	45.3	290	5	US-10-721-922A-96	Sequence 96, Appl	467	34	45.3	500	5	US-10-989-891-145	Sequence 145, App
395	34	45.3	296	4	US-10-153-668-57	Sequence 57, Appl	468	34	45.3	501	5	US-10-369-493-11711	Sequence 21711, A
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399	34	45.3	305	3	US-09-804-291-501	Sequence 501, App	472	34	45.3	523	5	US-10-732-923-4483	Sequence 4483, App
400	34	45.3	305	4	US-10-387-629-224	Sequence 224, App	473	34	45.3	523	5	US-10-732-923-18769	Sequence 18769, A
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402	34	45.3	305	5	US-10-819-316-501	Sequence 501, App	475	34	45.3	544	3	US-09-925-299-1004	Sequence 1004, App
403	34	45.3	310	5	US-10-773-236-349	Sequence 349, App	476	34	45.3	544	3	US-09-925-299-1004	Sequence 1004, App
404	34	45.3	322	4	US-10-437-963-127975	Sequence 127975, A	477	34	45.3	546	4	US-10-112-944-112	Sequence 712, App
405	34	45.3	322	4	US-10-437-963-173243	Sequence 173243, A	478	34	45.3	546	5	US-10-450-763-40380	Sequence 40380, App
406	34	45.3	325	5	US-10-494-675-56	Sequence 56, Appl	479	34	45.3	553	4	US-10-282-122A-17764	Sequence 47764, A
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410	34	45.3	357	5	US-10-501-282-5452	Sequence 5452, App	483	34	45.3	582	3	US-09-738-626-5406	Sequence 5406, App
411	34	45.3	360	4	US-10-437-963-155373	Sequence 155373, A	484	34	45.3	608	4	US-10-411-910A-16	Sequence 16, Appl
412	34	45.3	361	4	US-10-282-122A-75545	Sequence 75545, A	485	34	45.3	620	4	US-10-369-493-3659	Sequence 3659, App
413	34	45.3	362	3	US-09-815-242-13954	Sequence 13954, A	486	34	45.3	627	4	US-10-425-115-274872	Sequence 274872, A
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421	34	45.3	381	4	US-10-425-115-237632	Sequence 237632, A	494	34	45.3	685	4	US-10-146-474-14	Sequence 14, Appl
422	34	45.3	383	4	US-10-344-738-2	Sequence 2, Appl1	495	34	45.3	685	5	US-10-301-764-14	Sequence 14, Appl
423	34	45.3	392	4	US-10-369-493-4381	Sequence 4381, App	496	34	45.3	685	5	US-10-882-586A-9	Sequence 9, Appl
424	34	45.3	392	4	US-10-369-493-7135	Sequence 7135, App	497	34	45.3	694	3	US-09-847-102A-56	Sequence 56, Appl
425	34	45.3	393	3	US-09-364-847-2	Sequence 2, Appl1	498	34	45.3	694	4	US-10-205-823-144	Sequence 144, App
426	34	45.3	393	4	US-10-282-122A-50631	Sequence 50631, A	499	34	45.3	694	4	US-10-285-976-53	Sequence 53, Appl
427	34	45.3	393	4	US-10-357-521-13	Sequence 13, Appl	500	34	45.3	694	4	US-10-295-027-1344	Sequence 1344, App
428	34	45.3	393	4	US-10-437-963-15758	Sequence 150758, A	501	34	45.3	694	4	US-10-311-623-6	Sequence 6, Appl1
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436	34	45.3	409	4	US-10-425-114-37813	Sequence 37813, A	509	34	45.3	740	5	US-10-408-765A-1280	Sequence 1280, App
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449	34	45.3	450	4	US-10-424-599-177153	Sequence 177153, A	522	34	45.3	1072	4	US-10-210-152-24	Sequence 24, Appl
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464	34	45.3	500	4	US-10-005-956-28	Sequence 28, Appl	537	34	45.3	1237	4	US-10-024-663-32	Sequence 32, Appl
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SUMMARIES

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24	75	100.0	2351	1	US-08-366-851A-2
25	75	100.0	2351	2	US-10-133-907-4
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31	56	74.7	16	1	US-08-488-379-170	Sequence 170, App
32	56	74.7	16	2	US-08-475-399A-170	Sequence 170, App
33	56	74.7	16	2	US-08-077-255A-170	Sequence 170, App
34	56	74.7	16	4	PCT-US93-07545-170	Sequence 170, App
35	56	74.7	868	1	US-07-864-004B-6	Sequence 6, Appli
36	56	74.7	868	1	US-08-251-937A-6	Sequence 6, Appli
37	56	74.7	868	1	US-08-212-133A-3	Sequence 6, Appli
38	56	74.7	1090	4	PCT-US93-03275-6	Sequence 6, Appli
39	56	74.7	1443	3	US-08-670-707A-39	Sequence 39, Appli
40	56	74.7	1443	3	US-09-037-601-39	Sequence 39, Appli
41	56	74.7	1443	3	US-09-315-179-39	Sequence 39, Appli
42	56	74.7	1467	2	US-09-523-656-38	Sequence 38, Appli
43	56	74.7	2115	2	US-09-324-867-5	Sequence 5, Appli
44	56	74.7	2133	1	US-08-670-707A-37	Sequence 37, Appli
45	56	74.7	2133	1	US-09-037-601-37	Sequence 37, Appli
46	56	74.7	2133	2	US-09-315-179-37	Sequence 37, Appli
47	56	74.7	2133	2	US-09-523-656-30	Sequence 30, Appli
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49	43	57.3	2319	1	US-08-212-133A-8	Sequence 8, Appli
50	43	57.3	2319	1	US-08-474-503-6	Sequence 6, Appli
51	43	57.3	2319	1	US-08-670-707A-6	Sequence 6, Appli
52	43	57.3	2319	2	US-09-037-601-6	Sequence 6, Appli
53	43	57.3	2319	2	US-09-315-179-6	Sequence 6, Appli
54	43	57.3	2319	2	US-09-523-656-28	Sequence 28, Appli
55	43	57.3	2319	4	PCT-US94-13200-6	Sequence 6, Appli
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58	39	52.0	315	2	US-09-438-185A-26	Sequence 26, Appli
59	38.5	51.3	445	2	US-09-270-767-45180	Sequence 45180, A
60	38.5	51.3	611	2	US-09-266-965-119	Sequence 119, App
61	38	50.7	151	2	US-09-252-991A-28213	Sequence 28213, A
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63	38	50.7	302	1	US-09-453-387A-6	Sequence 6, Appli
64	38	50.7	2414	1	US-08-227-536-2	Sequence 2, Appli
65	38	50.7	2414	2	US-09-538-092-1289	Sequence 1289, Ap
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68	38	50.7	2441	1	US-08-961-739-2	Sequence 2, Appli
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83	36	48.0	324	2	US-09-270-767-45894	Sequence 45894, A
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89	36	48.0	413	2	US-09-540-236-1208	Sequence 3208, Ap
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96	35	46.7	147	2	US-09-252-991A-24937	Sequence 24937, A
97	35	46.7	180	2	US-09-640-211A-834	Sequence 834, App
98	35	46.7	187	2	US-09-583-110-801	Sequence 4801, Ap
99	35	46.7	190	2	US-09-107-433-4832	Sequence 4832, Ap
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103	35	46.7	341	2	US-09-248-796A-19160	Sequence 19160, A	176	34	45.3	1182	2	US-09-060-939A-7	Sequence 7, Appl1
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105	35	46.7	345	1	US-07-954-840A-10	Sequence 10, Appl1	178	34	45.3	1213	1	US-08-646-715-20	Sequence 20, Appl1
106	35	46.7	345	1	US-07-954-840A-12	Sequence 12, Appl1	179	34	45.3	1430	2	US-09-252-991A-18190	Sequence 18190, A
107	35	46.7	345	1	US-07-954-840A-16	Sequence 16, Appl1	180	33.5	44.7	389	2	US-09-712-353-196	Sequence 196, App
108	35	46.7	345	1	US-07-954-840A-18	Sequence 18, Appl1	181	33	44.0	102	2	US-09-634-228-347	Sequence 347, App
109	35	46.7	345	1	US-07-954-840A-20	Sequence 20, Appl1	182	33	44.0	118	2	US-09-270-767-61948	Sequence 61948, A
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111	35	46.7	345	1	US-07-954-840A-24	Sequence 24, Appl1	184	33	44.0	193	2	US-09-513-999C-5047	Sequence 5047, Ap
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113	35	46.7	345	1	US-07-954-840A-31	Sequence 31, Appl1	186	33	44.0	209	2	US-09-252-991A-17166	Sequence 17166, A
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116	35	46.7	347	1	US-07-954-840A-6	Sequence 6, Appl1	189	33	44.0	298	2	US-09-711-164-352	Sequence 352, App
117	35	46.7	347	1	US-07-954-840A-8	Sequence 8, Appl1	190	33	44.0	304	2	US-09-252-991A-32503	Sequence 32503, A
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126	35	46.7	585	1	US-09-169-027-11	Sequence 11, Appl1	199	33	44.0	388	2	US-08-446-822-8	Sequence 8, Appl1
127	35	46.7	586	1	US-08-453-848-19	Sequence 19, Appl1	200	33	44.0	388	2	US-09-328-314-8	Sequence 8, Appl1
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130	35	46.7	592	2	US-09-169-027-17	Sequence 17, Appl1	203	33	44.0	388	4	PCT-US93-12586-8	Sequence 8, Appl1
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136	35	46.7	1813	2	US-09-949-016-8284	Sequence 8284, Ap	209	33	44.0	415	2	US-09-270-767-56686	Sequence 56686, A
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141	34	45.3	56	2	US-09-513-999C-6081	Sequence 6081, Ap	214	33	44.0	492	2	US-10-104-047-3323	Sequence 3323, Ap
142	34	45.3	85	2	US-09-621-976-7043	Sequence 7043, Ap	215	33	44.0	497	2	US-09-252-991A-23670	Sequence 23670, A
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155	34	45.3	393	2	US-08-178-257-13	Sequence 13, Appl1	228	33	44.0	775	1	US-07-603-133B-14	Sequence 14, Appl1
156	34	45.3	393	2	US-09-607-123-6	Sequence 6, Appl1	229	33	44.0	997	1	US-08-232-540-1	Sequence 1, Appl1
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169	34	45.3	589	2	US-09-169-027-13	Sequence 13, Appl1	242	33	44.0	1619	2	US-09-949-016-9450	Sequence 9450, Ap
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171	34	45.3	715	2	US-10-104-047-3385	Sequence 3385, Ap	244	32	42.7	18	2	US-07-795-859B-16	Sequence 16, Appl1
172	34	45.3	740	2	US-09-022-983-5	Sequence 5, Appl1	245	32	42.7	34	1	US-08-457-616-16	Sequence 16, Appl1
173	34	45.3	742	2	US-09-949-016-11569	Sequence 11569, A	246	32	42.7	34	1	US-08-457-616-16	Sequence 16, Appl1

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260	32	42.7	239	2	US-09-709-791-4	Sequence 4, App1
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262	32	42.7	243	2	US-08-634-475-5	Sequence 5, App1
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265	32	42.7	255	1	US-08-457-616-2	Sequence 2, App1
266	32	42.7	259	1	US-07-795-859B-4	Sequence 4, App1
267	32	42.7	259	1	US-08-457-616-4	Sequence 4, App1
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273	32	42.7	289	2	US-09-068-804-40	Sequence 40, App1
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285	32	42.7	340	2	US-09-188-930-184	Sequence 184, App
286	32	42.7	340	2	US-09-312-283C-184	Sequence 184, App
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295	32	42.7	374	2	US-09-540-236-2230	Sequence 2230, App
296	32	42.7	393	2	US-09-377-557-17	Sequence 17, App1
297	32	42.7	397	2	US-08-178-257-14	Sequence 17, App1
298	32	42.7	403	2	US-09-602-787A-606	Sequence 606, App
299	32	42.7	408	2	US-09-248-796A-19407	Sequence 19407, A
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303	32	42.7	419	2	US-09-270-767-46031	Sequence 46031, A
304	32	42.7	423	2	US-09-438-917-16	Sequence 16, App1
305	32	42.7	429	2	US-09-252-991A-51821	Sequence 51821, A
306	32	42.7	440	2	US-08-759-628-4	Sequence 4, App1
307	32	42.7	450	2	US-09-252-991A-18822	Sequence 18822, A
308	32	42.7	465	2	US-09-902-540-12612	Sequence 12612, A
309	32	42.7	465	2	US-09-199-637A-29	Sequence 29, App1
310	32	42.7	468	2	US-09-543-681A-671	Sequence 4671, App
311	32	42.7	484	2	US-09-248-796A-16180	Sequence 16180, A
312	32	42.7	485	2	US-09-270-767-43385	Sequence 43385, A
313	32	42.7	493	2	US-09-248-796A-16445	Sequence 16445, A
314	32	42.7	494	2	US-09-270-767-42129	Sequence 42129, A
315	32	42.7	497	2	US-09-377-557-10	Sequence 10, App1
316	32	42.7	510	2	US-09-252-991A-17695	Sequence 17695, A
317	32	42.7	510	2	US-09-564-808-6	Sequence 6, App1
318	32	42.7	519	1	US-08-725-736D-2	Sequence 2, App1
319	32	42.7	519	2	US-09-162-360B-2	Sequence 2, App1
320	32	42.7	519	2	US-09-161-877B-2	Sequence 2, App1
321	32	42.7	519	2	US-09-248-796A-14534	Sequence 14534, A
322	32	42.7	519	2	US-09-949-016-6144	Sequence 6144, App
323	32	42.7	526	2	US-09-252-991A-20120	Sequence 20120, A
324	32	42.7	550	2	US-09-949-016-9886	Sequence 9886, App
325	32	42.7	564	2	US-09-252-991A-26990	Sequence 26990, A
326	32	42.7	576	2	US-09-248-796A-20352	Sequence 20352, A
327	32	42.7	586	2	US-09-538-106-22	Sequence 22, App1
328	32	42.7	592	2	US-09-614-912-80	Sequence 90, App1
329	32	42.7	593	1	US-08-591-079-8	Sequence 8, App1
330	32	42.7	593	1	US-08-591-079-10	Sequence 10, App1
331	32	42.7	627	2	US-09-489-039A-12782	Sequence 12782, A
332	32	42.7	680	2	US-09-538-106-19	Sequence 19, App1
333	32	42.7	681	2	US-10-158-847-140	Sequence 140, App
334	32	42.7	681	2	US-10-158-825-140	Sequence 140, App
335	32	42.7	694	2	US-09-248-796A-20618	Sequence 20618, A
336	32	42.7	711	2	US-10-158-847-138	Sequence 138, App
337	32	42.7	711	2	US-10-158-825-138	Sequence 138, App
338	32	42.7	719	2	US-09-252-991A-30052	Sequence 30052, A
339	32	42.7	720	2	US-09-857-556A-26	Sequence 26, App1
340	32	42.7	735	2	US-10-104-047-3774	Sequence 3774, App
341	32	42.7	739	2	US-09-487-558B-396	Sequence 396, App
342	32	42.7	744	1	US-08-764-100-25	Sequence 25, App
343	32	42.7	772	2	US-09-252-991A-30121	Sequence 30121, A
344	32	42.7	783	2	US-09-252-991A-18035	Sequence 18035, A
345	32	42.7	805	2	US-08-989-299-2	Sequence 2, App1
346	32	42.7	805	2	US-10-158-847-142	Sequence 142, App
347	32	42.7	805	2	US-09-407-427-2	Sequence 2, App1
348	32	42.7	805	2	US-09-635-501-2	Sequence 2, App1
349	32	42.7	805	2	US-09-635-501-106	Sequence 106, App
350	32	42.7	805	2	US-10-158-825-142	Sequence 142, App
351	32	42.7	819	2	US-09-949-016-11284	Sequence 11284, A
352	32	42.7	838	2	US-09-252-991A-25809	Sequence 25809, A
353	32	42.7	840	2	US-09-489-039A-11722	Sequence 11722, A
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355	32	42.7	891	2	US-10-104-047-2992	Sequence 2992, App
356	32	42.7	891	2	US-10-028-056-4	Sequence 4, App1
357	32	42.7	903	2	US-09-270-767-6470	Sequence 4670, A
358	32	42.7	924	2	US-10-028-056-5	Sequence 5, App1
359	32	42.7	1036	2	US-09-543-681A-7736	Sequence 7736, App
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361	32	42.7	1064	2	US-09-626-301-4	Sequence 4, App1
362	32	42.7	1137	2	US-09-902-481B-3	Sequence 3, App1
363	32	42.7	1137	2	US-09-902-481B-4	Sequence 4, App1
364	32	42.7	1137	2	US-09-902-481B-5	Sequence 5, App1
365	32	42.7	1137	2	US-09-902-481B-6	Sequence 6, App1
366	32	42.7	1152	1	US-08-476-062A-43	Sequence 43, App1
367	32	42.7	1152	4	PCR-US96-01314-43	Sequence 43, App1
368	32	42.7	1152	6	PCT-US96-01314-43	Sequence 43, App1
369	32	42.7	1153	1	US-08-173-497-3	Sequence 3, App1
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371	32	42.7	1153	1	US-08-485-618-3	Sequence 3, App1
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373	32	42.7	1153	1	US-08-605-672-3	Sequence 3, App1
374	32	42.7	1153	1	US-08-482-293A-3	Sequence 3, App1
375	32	42.7	1153	1	US-08-943-363-3	Sequence 3, App1
376	32	42.7	1153	2	US-09-193-043-3	Sequence 3, App1
377	32	42.7	1153	2	US-09-688-307A-3	Sequence 3, App1
378	32	42.7	1153	2	US-09-350-259-3	Sequence 3, App1
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380	32	42.7	1177	2	US-09-795-927-2	Sequence 2, App1
381	32	42.7	1197	2	US-09-618-425-2	Sequence 2, App1
382	32	42.7	1871	2	US-09-964-966-42	Sequence 42, App1
383	32	42.7	3118	1	US-08-457-273B-8	Sequence 8, App1
384	32	42.7	3119	1	US-08-246-962A-16	Sequence 16, App1
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386	32	42.7	3210	2	US-09-538-092-1154	Sequence 1154, App
387	32	42.7	3248	1	US-08-353-700-1	Sequence 1, App1
388	32	42.7	3248	4	PCT-US95-16216-1	Sequence 1, App1
389	31.5	42.0	3248	4	US-09-252-991A-20542	Sequence 20542, A
390	31.5	42.0	168	2	US-09-252-991A-32502	Sequence 32502, A
391	31.5	42.0	191	2	US-10-101-464A-625	Sequence 625, App
392	31.5	42.0	360	2	US-09-847-057-2	Sequence 2, App1

393	31	41.3	32	2	US-09-716-964B-206	Sequence 206, App	466	31	41.3	256	2	US-09-248-796A-19223	Sequence 19223, A
394	31	41.3	57	1	US-09-621-976-7386	Sequence 7386, Ap	467	31	41.3	262	2	US-09-154-083-24	Sequence 244, Appl
395	31	41.3	59	2	US-08-488-961-3	Sequence 3, Appl1	468	31	41.3	270	2	US-09-107-532A-5444	Sequence 544, Ap
396	31	41.3	59	2	US-08-973-297-3	Sequence 3, Appl1	469	31	41.3	271	2	US-09-270-767-97528	Sequence 37528, A
397	31	41.3	59	2	US-09-632-957-3	Sequence 3, Appl1	470	31	41.3	271	2	US-09-270-767-97528	Sequence 37528, A
398	31	41.3	59	4	PCT-US86-06511-3	Sequence 3, Appl1	471	31	41.3	274	2	US-09-270-767-44349	Sequence 44349, A
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400	31	41.3	61	2	US-09-270-767-55165	Sequence 55165, A	473	31	41.3	278	2	US-09-252-991A-21348	Sequence 21348, A
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402	31	41.3	64	2	US-09-489-039A-8930	Sequence 8930, Ap	475	31	41.3	283	2	US-10-012-211A-111	Sequence 11, App
403	31	41.3	64	2	US-09-489-039A-11358	Sequence 11358, A	476	31	41.3	283	2	US-10-015-789A-111	Sequence 11, App
404	31	41.3	66	2	US-09-328-352-6470	Sequence 6470, Ap	477	31	41.3	283	2	US-10-006-768A-111	Sequence 11, App
405	31	41.3	81	2	US-09-621-976-6334	Sequence 6334, Ap	478	31	41.3	283	2	US-10-015-671A-111	Sequence 11, App
406	31	41.3	87	2	US-09-621-976-7558	Sequence 7558, Ap	479	31	41.3	283	2	US-10-015-333A-111	Sequence 11, App
407	31	41.3	87	2	US-09-471-276-1389	Sequence 1389, Ap	480	31	41.3	283	2	US-10-011-833A-111	Sequence 11, App
408	31	41.3	92	2	US-09-248-796A-24553	Sequence 24553, A	481	31	41.3	283	2	US-10-006-041A-111	Sequence 11, App
409	31	41.3	96	2	US-09-621-976-6037	Sequence 6037, Ap	482	31	41.3	283	2	US-10-012-064A-111	Sequence 11, App
410	31	41.3	101	2	US-09-198-452A-1193	Sequence 1193, Ap	483	31	41.3	289	2	US-09-710-279-1254	Sequence 3254, App
411	31	41.3	101	2	US-09-716-129-80	Sequence 80, Appl	484	31	41.3	306	2	US-09-252-991A-19132	Sequence 19132, A
412	31	41.3	108	2	US-08-858-207A-327	Sequence 327, App	485	31	41.3	309	2	US-09-949-016-6192	Sequence 81932, Ap
413	31	41.3	108	2	US-09-438-185A-434	Sequence 434, App	486	31	41.3	316	2	US-09-252-991A-18153	Sequence 18153, A
414	31	41.3	124	2	US-09-621-976-4006	Sequence 4006, Ap	487	31	41.3	319	2	US-09-758-759-69	Sequence 89, Appl
415	31	41.3	125	1	US-08-534-975-5	Sequence 5, Appl1	488	31	41.3	322	2	US-09-303-518D-130	Sequence 130, App
416	31	41.3	125	1	US-08-954-470-5	Sequence 5, Appl1	489	31	41.3	327	2	US-09-008-271A-10	Sequence 10, Appl
417	31	41.3	125	1	US-08-306-511A-6	Sequence 6, Appl1	490	31	41.3	327	2	US-09-968-415-10	Sequence 10, Appl
418	31	41.3	125	1	US-08-893-274-6	Sequence 6, Appl1	491	31	41.3	332	2	US-09-248-796A-17382	Sequence 17382, A
419	31	41.3	125	2	US-08-581-918A-6	Sequence 6, Appl1	492	31	41.3	366	2	US-09-252-991A-23504	Sequence 23504, A
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421	31	41.3	125	2	US-09-247-154-5	Sequence 5, Appl1	494	31	41.3	375	2	US-09-252-991A-24278	Sequence 24278, A
422	31	41.3	125	2	US-08-346-147B-6	Sequence 6, Appl1	495	31	41.3	379	2	US-09-710-279-2810	Sequence 2810, Ap
423	31	41.3	125	2	US-08-822-936-6	Sequence 6, Appl1	496	31	41.3	385	2	US-09-517-779-4	Sequence 4, Appl1
424	31	41.3	125	2	US-08-497-214D-6	Sequence 6, Appl1	497	31	41.3	390	2	US-09-902-540-14589	Sequence 14589, Ap
425	31	41.3	125	2	US-09-480-718-5	Sequence 5, Appl1	498	31	41.3	399	2	US-09-134-001C-4567	Sequence 4567, Ap
426	31	41.3	125	2	US-09-610-833-5	Sequence 5, Appl1	499	31	41.3	405	2	US-09-166-265-1	Sequence 1, Appl1
427	31	41.3	125	2	US-09-016-750C-6	Sequence 6, Appl1	500	31	41.3	410	2	US-09-252-991A-25812	Sequence 25812, A
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431	31	41.3	127	2	US-08-346-147B-14	Sequence 14, Appl	504	31	41.3	436	2	US-09-712-353-558	Sequence 255, App
432	31	41.3	127	2	US-08-497-214D-14	Sequence 14, Appl	505	31	41.3	440	2	US-09-902-540-15770	Sequence 15770, A
433	31	41.3	127	2	US-09-016-750C-14	Sequence 14, Appl	506	31	41.3	444	2	US-09-949-016-9537	Sequence 9537, Ap
434	31	41.3	132	2	US-09-716-129-179	Sequence 179, App	507	31	41.3	446	1	US-08-874-138-6	Sequence 6, Appl1
435	31	41.3	134	2	US-09-621-976-4005	Sequence 4005, Ap	508	31	41.3	446	2	US-08-879-941-2	Sequence 2, Appl1
436	31	41.3	137	2	US-09-252-991A-21684	Sequence 21684, A	509	31	41.3	446	2	US-09-747-116-2	Sequence 2, Appl1
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438	31	41.3	145	2	US-09-489-039A-8687	Sequence 8687, Ap	511	31	41.3	457	2	US-09-252-991A-25211	Sequence 25211, A
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441	31	41.3	147	2	US-09-270-767-48528	Sequence 48528, A	514	31	41.3	461	2	US-09-043-944-6	Sequence 6, Appl1
442	31	41.3	151	2	US-09-601-729-16	Sequence 16, Appl	515	31	41.3	461	2	US-10-811-159-6	Sequence 1, Appl1
443	31	41.3	151	2	US-09-893-737-102	Sequence 102, App	516	31	41.3	461	2	US-10-811-159-6	Sequence 6, Appl1
444	31	41.3	165	2	US-08-311-731A-279	Sequence 279, App	517	31	41.3	465	2	US-10-029-180-44	Sequence 44, Appl
445	31	41.3	167	1	US-08-627-610-6	Sequence 6, Appl1	518	31	41.3	483	2	US-09-252-991A-19224	Sequence 19224, A
446	31	41.3	168	1	US-08-508-735-46	Sequence 46, Appl	519	31	41.3	484	2	US-10-142-221-56	Sequence 56, Appl
447	31	41.3	168	2	US-09-201-139-46	Sequence 46, Appl	520	31	41.3	493	2	US-09-248-796A-17545	Sequence 17545, A
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449	31	41.3	172	2	US-09-270-767-48723	Sequence 48723, A	522	31	41.3	495	2	US-09-252-991A-32802	Sequence 32802, A
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455	31	41.3	221	1	US-09-252-991A-18985	Sequence 18985, A	528	31	41.3	528	2	US-09-252-991A-22551	Sequence 22551, A
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458	31	41.3	226	2	US-09-134-001C-5556	Sequence 5556, Ap	531	31	41.3	573	2	US-09-252-991A-18744	Sequence 18744, A
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463	31	41.3	249	2	US-08-591-468-2	Sequence 2, Appl1	536	31	41.3	616	2	US-09-489-039A-9231	Sequence 9231, Ap
464	31	41.3	249	2	US-09-650-324A-38	Sequence 38, Appl	537	31	41.3	624	2	US-09-538-032-227	Sequence 227, App
465	31	41.3	249	4	US-10-039-112A-38	Sequence 38, Appl	538	31	41.3	633	2	US-09-949-016-10337	Sequence 10337, A
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540	31	41.3	657	2	US-09-489-039A-13360	Sequence 13360, A	613	30	40.0	105	2	US-10-101-464A-523	Sequence 523, App
541	31	41.3	663	2	US-09-949-016-6046	Sequence 6046, Ap	614	30	40.0	107	2	US-09-902-540-13200	Sequence 13200, A
542	31	41.3	666	2	US-10-104-047-3618	Sequence 3618, Ap	615	30	40.0	115	2	US-09-463-931-2	Sequence 2, Appli
543	31	41.3	673	2	US-09-949-016-7834	Sequence 7834, Ap	616	30	40.0	116	2	US-09-252-991A-21035	Sequence 21035, A
544	31	41.3	710	2	US-10-087-042-15	Sequence 15, Appl	617	30	40.0	116	2	US-09-543-681A-5338	Sequence 5338, Ap
545	31	41.3	721	2	US-09-949-016-11031	Sequence 11031, A	618	30	40.0	116	2	US-09-438-185A-513	Sequence 513, App
546	31	41.3	720	2	US-09-543-681A-5220	Sequence 5220, Ap	619	30	40.0	127	2	US-09-270-767-00383	Sequence 60383, A
547	31	41.3	736	2	US-09-252-991A-3226	Sequence 3226, A	620	30	40.0	130	2	US-09-270-767-11728	Sequence 31728, A
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549	31	41.3	897	2	US-10-104-047-2474	Sequence 2474, Ap	622	30	40.0	132	2	US-09-228-986-110	Sequence 110, App
550	31	41.3	942	2	US-08-328-322-5	Sequence 5, Appli	623	30	40.0	133	2	US-10-101-464A-110	Sequence 110, App
551	31	41.3	915	2	US-09-538-092-602	Sequence 602, App	624	30	40.0	133	2	US-09-252-991A-16838	Sequence 16838, A
552	31	41.3	980	1	US-08-091-569-2	Sequence 2, Appli	625	30	40.0	145	2	US-09-640-210A-698	Sequence 698, App
553	31	41.3	980	1	US-08-203-676-2	Sequence 2, Appli	626	30	40.0	147	2	US-09-248-786A-20089	Sequence 20089, A
554	31	41.3	980	1	US-08-822-238-2	Sequence 2, Appli	627	30	40.0	152	2	US-09-270-767-1847	Sequence 31847, A
555	31	41.3	1012	2	US-08-126-505A-15	Sequence 15, Appl	628	30	40.0	152	2	US-09-270-767-47064	Sequence 47064, A
556	31	41.3	1016	2	US-09-949-016-11304	Sequence 11304, A	629	30	40.0	155	2	US-09-489-039A-11168	Sequence 11168, A
557	31	41.3	1033	2	US-09-834-309-1	Sequence 1, Appli	630	30	40.0	158	2	US-09-270-767-17557	Sequence 37557, A
558	31	41.3	1066	2	US-09-252-991A-11550	Sequence 31550, A	631	30	40.0	158	2	US-09-270-767-52774	Sequence 52774, A
559	31	41.3	1068	2	US-09-085-199B-11	Sequence 11, Appl	632	30	40.0	162	2	US-09-270-767-16816	Sequence 36816, A
560	31	41.3	1085	1	US-08-431-080-28	Sequence 28, Appl	633	30	40.0	162	2	US-09-270-767-52033	Sequence 52033, A
561	31	41.3	1085	1	US-08-938-534-28	Sequence 28, Appl	634	30	40.0	165	2	US-09-252-991A-19490	Sequence 19490, A
562	31	41.3	1085	2	US-09-345-294-28	Sequence 28, Appl	635	30	40.0	177	2	US-08-737-248-21	Sequence 21, Appl
563	31	41.3	1093	2	US-09-487-558B-192	Sequence 392, App	636	30	40.0	181	2	US-09-134-000C-4467	Sequence 4467, Ap
564	31	41.3	1151	2	US-09-252-991A-21328	Sequence 21328, A	637	30	40.0	184	2	US-09-270-767-43502	Sequence 43502, A
565	31	41.3	1193	2	US-09-227-725A-4	Sequence 4, Appli	638	30	40.0	202	2	US-09-370-858-38	Sequence 38, Appl
566	31	41.3	1193	2	US-10-071-900-4	Sequence 4, Appli	639	30	40.0	202	2	US-09-854-133-38	Sequence 38, Appl
567	31	41.3	1211	2	US-09-167-206-14	Sequence 14, Appl	640	30	40.0	203	6	5168051-12	Patent No. 5168051
568	31	41.3	1237	2	US-09-862-027-78	Sequence 78, Appl	641	30	40.0	204	1	US-08-155-171B-20	Sequence 20, Appl
569	31	41.3	1588	1	US-08-698-551-16	Sequence 16, Appl	642	30	40.0	204	1	US-08-435-998-80	Sequence 11279, A
570	31	41.3	1588	1	US-08-603-228-16	Sequence 16, Appl	643	30	40.0	205	2	US-09-902-540-11279	Sequence 11279, A
571	31	41.3	1588	1	US-08-835-032A-16	Sequence 16, Appl	644	30	40.0	206	2	US-09-270-767-43027	Sequence 43027, A
572	31	41.3	1588	2	US-09-185-258C-16	Sequence 16, Appl	645	30	40.0	208	2	US-09-248-766A-17907	Sequence 17907, A
573	31	41.3	1588	2	US-09-976-594-965	Sequence 965, App	646	30	40.0	211	2	US-09-252-991A-25509	Sequence 25509, A
574	31	41.3	1688	2	US-10-042-665A-7	Sequence 7, Appli	647	30	40.0	212	2	US-09-270-767-42034	Sequence 32034, A
575	31	41.3	1703	2	US-09-824-574-3	Sequence 3, Appli	648	30	40.0	212	2	US-09-270-767-47251	Sequence 47251, A
576	31	41.3	1703	2	US-09-487-558B-40	Sequence 340, App	649	30	40.0	213	2	US-09-902-540-10255	Sequence 10255, A
577	31	41.3	1721	2	US-10-042-665A-6	Sequence 6, Appli	650	30	40.0	227	2	US-09-461-325-211	Sequence 211, App
578	31	41.3	1792	2	US-09-561-818A-12	Sequence 12, Appl	651	30	40.0	227	2	US-10-012-342-211	Sequence 211, App
579	31	41.3	1816	2	US-09-561-818A-10	Sequence 10, Appl	652	30	40.0	227	2	US-10-115-123-311	Sequence 211, App
580	31	41.3	1990	2	US-09-902-540-11251	Sequence 11251, A	653	30	40.0	228	2	US-09-270-767-44420	Sequence 44420, A
581	31	41.3	2183	2	US-08-746-111-5	Sequence 5, Appli	654	30	40.0	230	2	US-09-248-766A-26509	Sequence 26509, A
582	31	41.3	2442	2	US-09-514-247A-10	Sequence 10, Appl	655	30	40.0	248	2	US-09-513-057C-29	Sequence 29, Appl
583	31	41.3	2442	2	US-09-538-092-1170	Sequence 1370, Ap	656	30	40.0	248	2	US-09-328-352-7658	Sequence 7658, Ap
584	31	41.3	2766	2	US-09-964-956-62	Sequence 62, Appl	657	30	40.0	248	2	US-09-746-801A-29	Sequence 29, Appl
585	31	41.3	3413	2	US-10-042-665A-8	Sequence 8, Appli	658	30	40.0	248	2	US-10-719-885-29	Sequence 29, Appl
586	31	41.3	5069	2	US-10-042-665A-5	Sequence 5, Appli	659	30	40.0	250	2	US-09-167-717-1	Sequence 1, Appli
587	30.5	40.7	186	2	US-09-501-115-16	Sequence 16, Appl	660	30	40.0	250	2	US-09-252-991A-24075	Sequence 24075, A
588	30.5	40.7	186	2	US-10-357-886-16	Sequence 16, Appl	661	30	40.0	250	2	US-10-104-067-2577	Sequence 2577, Ap
589	30.5	40.7	292	2	US-10-104-047-2862	Sequence 2862, Ap	662	30	40.0	252	2	US-09-340-236-3340	Sequence 2340, Ap
590	30.5	40.7	337	1	US-09-057-762-2	Sequence 2, Appli	663	30	40.0	252	2	US-09-270-767-44107	Sequence 44107, A
591	30.5	40.7	337	2	US-08-326-119A-2	Sequence 2, Appli	664	30	40.0	253	2	US-09-252-991A-27487	Sequence 27487, A
592	30.5	40.7	376	2	US-09-025-691-3	Sequence 3, Appli	665	30	40.0	258	2	US-09-684-938-181	Sequence 181, App
593	30.5	40.7	1984	2	US-08-836-325-10	Sequence 10, Appl	666	30	40.0	258	2	US-09-308-825A-181	Sequence 181, App
594	30.5	40.7	1984	2	US-09-457-571-10	Sequence 10, Appl	667	30	40.0	258	2	US-09-940-244-261	Sequence 261, App
595	30.5	40.7	1989	2	US-08-836-325-12	Sequence 12, Appl	668	30	40.0	271	2	US-09-270-767-42656	Sequence 42656, A
596	30.5	40.7	1989	2	US-09-457-571-12	Sequence 12, Appl	669	30	40.0	274	2	US-09-252-991A-23302	Sequence 23302, A
597	30	40.0	22	2	US-09-205-258-289	Sequence 289, App	670	30	40.0	275	2	US-09-557-170A-25	Sequence 25, Appl
598	30	40.0	22	2	US-10-004-860-289	Sequence 289, App	671	30	40.0	279	2	US-09-248-766A-17246	Sequence 17246, A
599	30	40.0	33	2	US-09-270-767-58863	Sequence 58863, A	672	30	40.0	283	2	US-09-377-557-6	Sequence 6, Appli
600	30	40.0	33	2	US-09-493-795B-300	Sequence 300, App	673	30	40.0	283	2	US-09-252-991A-27181	Sequence 27181, A
601	30	40.0	65	2	US-09-489-039A-11183	Sequence 11183, A	674	30	40.0	284	2	US-09-312-283C-389	Sequence 389, App
602	30	40.0	65	2	US-09-489-039A-11184	Sequence 11184, A	675	30	40.0	292	2	US-09-252-991A-18951	Sequence 18951, A
603	30	40.0	76	2	US-09-248-796A-23527	Sequence 23527, A	676	30	40.0	296	2	US-09-557-170A-27	Sequence 27, Appl
604	30	40.0	76	2	US-09-448-806C-9	Sequence 9, Appli	677	30	40.0	305	2	US-09-270-767-16407	Sequence 36407, A
605	30	40.0	78	2	US-09-270-767-58355	Sequence 58355, A	678	30	40.0	305	2	US-09-270-767-51624	Sequence 51624, A
606	30	40.0	80	2	US-09-530-903C-3	Sequence 3, Appli	679	30	40.0	309	2	US-09-603-208A-110	Sequence 110, App
607	30	40.0	89	2	US-09-187-789-15	Sequence 15, Appl	680	30	40.0	311	2	US-09-248-766A-27827	Sequence 27827, A
608	30	40.0	89	2	US-09-139-600-10	Sequence 10, Appl	681	30	40.0	315	2	US-09-134-001C-3561	Sequence 3561, App
609	30	40.0	89	2	US-09-989-903-15	Sequence 15, Appl	682	30	40.0	317	2	US-09-746-801A-57	Sequence 57, Appl
610	30	40.0	100	2	US-09-732-210-1168	Sequence 1168, Ap	683	30	40.0	317	2	US-10-719-885-57	Sequence 57, Appl
611	30	40.0	100	2	US-09-732-210-1171	Sequence 1171, Ap	684	30	40.0	323	2	US-09-252-991A-29711	Sequence 29711, A

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686	30	40.0	330	2	US-08-969-644-22	Sequence 22, Appl	759	30	40.0	465	2	US-09-949-016-1244	Sequence 7244, Ap
687	30	40.0	330	2	US-08-444-189-22	Sequence 22, Appl	760	30	40.0	470	1	US-08-471-496-2	Sequence 2, Appl
688	30	40.0	330	2	US-08-468-544-22	Sequence 22, Appl	761	30	40.0	470	1	US-08-894-840-2	Sequence 2, Appl
689	30	40.0	330	2	US-09-489-039A-11639	Sequence 11639, A	762	30	40.0	470	1	US-09-139-675-2	Sequence 2, Appl
690	30	40.0	331	2	US-09-489-847-309	Sequence 309, App	763	30	40.0	470	2	US-09-502-018-2	Sequence 2, Appl
691	30	40.0	333	2	US-09-252-991A-27785	Sequence 27785, A	764	30	40.0	471	2	US-09-252-991A-24511	Sequence 24511, A
692	30	40.0	336	2	US-09-131-648-1	Sequence 1, Appl	765	30	40.0	471	2	US-09-538-092-1295	Sequence 1295, Ap
693	30	40.0	336	2	US-09-543-681A-6586	Sequence 6586, Ap	766	30	40.0	476	1	US-08-958-713-4	Sequence 4, Appl
694	30	40.0	336	2	US-09-902-540-14259	Sequence 14259, A	767	30	40.0	476	2	US-09-328-352-5735	Sequence 6735, Ap
695	30	40.0	338	2	US-09-385-219A-12	Sequence 12, Appl	768	30	40.0	483	2	US-09-770-509-18	Sequence 18, Appl
696	30	40.0	338	2	US-09-949-016-11580	Sequence 11580, A	769	30	40.0	484	2	US-09-457-0408-12	Sequence 12, Appl
697	30	40.0	339	2	US-09-252-991A-28087	Sequence 28087, A	770	30	40.0	487	2	US-09-525-046-2	Sequence 2, Appl
698	30	40.0	339	2	US-09-107-532A-5514	Sequence 5514, Ap	771	30	40.0	489	2	US-09-949-016-9784	Sequence 9784, Ap
699	30	40.0	339	2	US-09-949-016-7598	Sequence 7598, Ap	772	30	40.0	497	2	US-08-956-11E-5234	Sequence 5234, Ap
700	30	40.0	341	2	US-09-538-092-305	Sequence 305, App	773	30	40.0	497	2	US-08-781-986A-5234	Sequence 5234, Ap
701	30	40.0	342	2	US-10-027-736A-71	Sequence 71, Appl	774	30	40.0	503	2	US-09-252-991A-2434	Sequence 2434, A
702	30	40.0	342	2	US-10-027-736A-72	Sequence 72, Appl	775	30	40.0	506	1	US-08-820-170A-19	Sequence 19, Appl
703	30	40.0	347	2	US-09-252-991A-19498	Sequence 19498, A	776	30	40.0	506	2	US-09-055-659-19	Sequence 19, Appl
704	30	40.0	349	2	US-09-543-681A-4507	Sequence 4507, Ap	777	30	40.0	506	2	US-09-273-565-19	Sequence 19, Appl
705	30	40.0	350	2	US-09-940-244-345	Sequence 345, App	778	30	40.0	506	2	US-09-565-538-19	Sequence 19, Appl
706	30	40.0	353	2	US-09-543-681A-6054	Sequence 6054, Ap	779	30	40.0	506	2	US-09-661-468-19	Sequence 19, Appl
707	30	40.0	354	2	US-09-232-200-55	Sequence 55, Appl	780	30	40.0	506	2	US-09-976-165-19	Sequence 19, Appl
708	30	40.0	354	2	US-09-232-197-55	Sequence 55, Appl	781	30	40.0	506	2	US-09-538-092-1381	Sequence 1381, Ap
709	30	40.0	354	2	US-09-232-201-55	Sequence 55, Appl	782	30	40.0	513	2	US-09-248-796A-15402	Sequence 15402, A
710	30	40.0	354	2	US-09-232-195-55	Sequence 55, Appl	783	30	40.0	514	2	US-09-248-796A-18586	Sequence 18586, A
711	30	40.0	359	2	US-09-902-540-16703	Sequence 16703, A	784	30	40.0	517	2	US-09-902-540-10229	Sequence 10229, A
712	30	40.0	361	2	US-09-786-240-32	Sequence 32, Appl	785	30	40.0	530	2	US-09-270-767-11545	Sequence 11545, A
713	30	40.0	365	2	US-10-027-736A-39	Sequence 39, Appl	786	30	40.0	532	2	US-09-949-016-6607	Sequence 6607, Ap
714	30	40.0	365	2	US-10-027-736A-30	Sequence 30, Appl	787	30	40.0	535	2	US-09-650-324A-62	Sequence 62, Appl
715	30	40.0	365	2	US-10-027-736A-64	Sequence 64, Appl	788	30	40.0	535	2	US-09-613-466-45	Sequence 45, Appl
716	30	40.0	372	2	US-09-252-991A-29108	Sequence 29108, A	789	30	40.0	535	2	US-10-039-112A-62	Sequence 62, Appl
717	30	40.0	373	2	US-08-908-436-2	Sequence 2, Appl	790	30	40.0	537	2	US-09-602-717A-46	Sequence 46, Appl
718	30	40.0	373	2	US-09-252-991A-19343	Sequence 19343, A	791	30	40.0	541	2	US-09-417-251A-8	Sequence 8, Appl
719	30	40.0	373	2	US-09-291-289-7	Sequence 7, Appl	792	30	40.0	541	2	US-09-902-540-10576	Sequence 10576, A
720	30	40.0	373	2	US-09-851-873-85	Sequence 85, Appl	793	30	40.0	545	2	US-09-248-796A-14961	Sequence 14961, A
721	30	40.0	376	2	US-09-248-796A-19997	Sequence 19997, A	794	30	40.0	547	2	US-09-252-991A-17749	Sequence 17749, A
722	30	40.0	383	2	US-09-252-991A-27087	Sequence 27087, A	795	30	40.0	549	2	US-10-104-047-3526	Sequence 3526, Ap
723	30	40.0	391	1	US-08-644-034A-1	Sequence 1, Appl	796	30	40.0	549	2	US-09-907-794A-259	Sequence 259, App
724	30	40.0	391	2	US-09-489-039A-9977	Sequence 9977, Ap	797	30	40.0	556	2	US-09-907-794A-259	Sequence 259, App
725	30	40.0	394	2	US-09-252-991A-28427	Sequence 28427, A	798	30	40.0	556	2	US-09-905-125A-259	Sequence 259, App
726	30	40.0	394	2	US-09-543-681A-5253	Sequence 5253, Ap	799	30	40.0	556	2	US-09-902-775A-259	Sequence 259, App
727	30	40.0	394	2	US-10-000-489-76	Sequence 76, Appl	800	30	40.0	556	2	US-09-906-700-259	Sequence 259, App
728	30	40.0	397	2	US-09-252-991A-25695	Sequence 25695, A	801	30	40.0	556	2	US-09-903-603A-259	Sequence 259, App
729	30	40.0	397	2	US-09-538-092-1116	Sequence 1116, Ap	802	30	40.0	556	2	US-09-904-920A-259	Sequence 259, App
730	30	40.0	403	2	US-09-270-767-44912	Sequence 44912, A	803	30	40.0	556	2	US-09-909-064-259	Sequence 259, App
731	30	40.0	410	4	PCT-US91-01861-3	Sequence 3, Appl	804	30	40.0	556	2	US-09-905-381A-259	Sequence 259, App
732	30	40.0	412	1	US-08-132-405-3	Sequence 3, Appl	805	30	40.0	556	2	US-09-906-618-259	Sequence 259, App
733	30	40.0	412	1	US-08-395-939A-3	Sequence 3, Appl	806	30	40.0	556	2	US-09-906-646-259	Sequence 259, App
734	30	40.0	412	2	US-09-380-662-21	Sequence 21, Appl	807	30	40.0	556	2	US-09-904-462-259	Sequence 259, App
735	30	40.0	412	2	US-09-949-016-6129	Sequence 6129, Ap	808	30	40.0	556	2	US-09-902-736A-259	Sequence 259, App
736	30	40.0	412	2	US-10-028-158-21	Sequence 21, Appl	809	30	40.0	556	2	US-09-906-722A-259	Sequence 259, App
737	30	40.0	412	2	US-09-756-283A-25	Sequence 25, Appl	810	30	40.0	557	2	US-09-889-463A-14	Sequence 14, Appl
738	30	40.0	412	4	PCT-US91-04541-2	Sequence 2, Appl	811	30	40.0	563	2	US-08-921-608A-3	Sequence 3, Appl
739	30	40.0	412	6	5262319-2	Patent No. 5262319	812	30	40.0	563	2	US-09-831-847-3	Sequence 3, Appl
740	30	40.0	413	2	US-09-949-016-7632	Sequence 7632, Ap	813	30	40.0	568	2	US-09-252-991A-22461	Sequence 22461, A
741	30	40.0	415	2	US-10-104-047-2254	Sequence 2254, Ap	814	30	40.0	573	2	US-09-270-767-33152	Sequence 33152, A
742	30	40.0	419	2	US-09-489-039A-12789	Sequence 12789, A	815	30	40.0	573	2	US-09-270-767-48369	Sequence 48369, A
743	30	40.0	422	2	US-09-347-878-26	Sequence 26, Appl	816	30	40.0	575	2	US-09-949-016-9760	Sequence 9760, Ap
744	30	40.0	424	2	US-09-252-991A-31825	Sequence 31825, A	817	30	40.0	585	2	US-09-134-000C-5945	Sequence 5945, Ap
745	30	40.0	424	2	US-09-491-577-88	Sequence 88, Appl	818	30	40.0	588	2	US-09-627-216A-14	Sequence 14, Appl
746	30	40.0	426	2	US-09-540-236-2053	Sequence 2053, Ap	819	30	40.0	588	2	US-09-765-873A-14	Sequence 14, Appl
747	30	40.0	428	2	US-09-949-016-6625	Sequence 6625, Ap	820	30	40.0	598	2	US-09-252-991A-20258	Sequence 20258, A
748	30	40.0	429	2	US-09-489-039A-12528	Sequence 12528, A	821	30	40.0	603	2	US-09-543-681A-6975	Sequence 6975, Ap
749	30	40.0	430	2	US-09-949-016-7361	Sequence 7361, Ap	822	30	40.0	605	2	US-09-489-039A-9333	Sequence 9333, Ap
750	30	40.0	433	2	US-09-949-016-8521	Sequence 8521, Ap	823	30	40.0	607	2	US-09-252-991A-30878	Sequence 30878, A
751	30	40.0	437	2	US-09-852-991A-18182	Sequence 18182, A	824	30	40.0	639	2	US-09-134-001C-5661	Sequence 5661, Ap
752	30	40.0	438	2	US-09-248-796A-19215	Sequence 19215, A	825	30	40.0	642	2	US-09-602-777A-44	Sequence 44, Appl
753	30	40.0	444	2	US-10-101-464A-733	Sequence 733, App	826	30	40.0	676	2	US-09-085-199B-7	Sequence 7, Appl
754	30	40.0	454	2	US-09-543-681A-4197	Sequence 4197, Ap	827	30	40.0	684	2	US-10-104-047-2418	Sequence 2418, Ap
755	30	40.0	455	2	US-09-270-767-44339	Sequence 44339, A	828	30	40.0	697	2	US-09-252-991A-24009	Sequence 24009, A
756	30	40.0	456	2	US-09-252-991A-26288	Sequence 26288, A	829	30	40.0	698	2	US-09-248-796A-19223	Sequence 19223, A
757	30	40.0	461	2	US-09-134-001C-3316	Sequence 3316, Ap	830	30	40.0	702	2	US-09-949-016-7288	Sequence 7288, Ap

831	30	40.0	709	2	US-09-543-681A-6114	Sequence 6114, Ap	904	30	40.0	1405	2	US-09-248-796A-18103	Sequence 18103, A
832	30	40.0	710	2	US-09-902-540-16023	Sequence 16023, A	905	30	40.0	1471	2	US-08-755-587-188	Sequence 188, App
833	30	40.0	730	1	US-07-846-181-5	Sequence 5, Appli	906	30	40.0	1566	2	US-09-581-472B-2	Sequence 2, Appli
834	30	40.0	730	1	US-07-845-989-5	Sequence 5, Appli	907	30	40.0	1581	2	US-09-110-517-2	Sequence 2, Appli
835	30	40.0	751	2	US-09-934-868-58	Sequence 58, Appl	908	30	40.0	1770	2	US-09-487-558B-298	Sequence 298, App
836	30	40.0	751	2	US-10-701-200-58	Sequence 58, Appl	909	30	40.0	1956	2	US-08-843-417-10	Sequence 10, Appl
837	30	40.0	760	2	US-09-513-057C-27	Sequence 27, Appl	910	30	40.0	1956	2	US-09-527-013-10	Sequence 10, Appl
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ALIGNMENTS

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RESULT 1
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; Sequence 1, Application US/09209916
; Patent No. 638703
; GENERAL INFORMATION:
; APPLICANT: Cho, Myung-Sam
; APPLICANT: Chan, Shun-Yuen
; APPLICANT: Kelsey, William
; APPLICANT: Yee, Helena
; TITLE OF INVENTION: Expression System for Factor VIII
; FILE REFERENCE: MSB-7255
; CURRENT APPLICATION NUMBER: US/09/209,916
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1438
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Derived from
US-09-209-916-1
; OTHER INFORMATION: human factor VIII sequence

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Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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RESULT 2
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; Sequence 3, Application US/09407605
; Patent No. 6924365
; GENERAL INFORMATION:
; APPLICANT: Selden, Richard F.
; APPLICANT: Miller, Allan M.
; APPLICANT: Treco, Douglas A.
; TITLE OF INVENTION: OPTIMIZED MESSENGER RNA
; FILE REFERENCE: 10278-009001
; CURRENT APPLICATION NUMBER: US/09/407,605

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CURRENT FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/130,241
PRIOR FILING DATE: 1999-04-20
PRIOR APPLICATION NUMBER: 60/102,239
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 136
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1445
TYPE: PRT
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US-09-407-605-3

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; RESULT 3
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; Sequence 4, Application US/09407605
; Patent No. 6924365
; GENERAL INFORMATION:
; APPLICANT: Selden, Richard F.
; APPLICANT: Miller, Allan M.
; APPLICANT: Treco, Douglas A.
; TITLE OF INVENTION: OPTIMIZED MESSENGER RNA
; FILE REFERENCE: 10278-009001
; CURRENT APPLICATION NUMBER: US/09/407,605
; CURRENT FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/130,241
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: 60/102,239
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 136
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; US-09-407-605-4

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; RESULT 4
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; Sequence 47, Application US/09001039B
; Patent No. 6818439
; GENERAL INFORMATION:
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Respass, James G.
; APPLICANT: DePolo, Nicholas J.
; APPLICANT: Hsu, David Chi-Tang
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Greengard, Judith
; APPLICANT: Lee, Will
; TITLE OF INVENTION: METHODS FOR ADMINISTRATION OF

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SUMMARIES

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64	39	52.0	784	2	O9U9R6_SCHMA	O9U9R6 schistosoma
65	39	52.0	784	2	O9Y1Y4_SCHMA	O9Y1Y4 schistosoma
66	39	52.0	918	2	O5LJPI_DROME	O5LJPI drosophila
67	39	52.0	982	2	O4RKM9_TETNG	O4RKM9 tetradon n
68	39	52.0	1078	2	O51YU8 MAGGR	O51Y8 magnaporthe
69	39	52.0	1096	2	O9F3J4_STRCO	O9F3J4 streptomyces
70	39	52.0	1336	2	O6FVJ1_CANGA	O6FVJ1 candida gla
71	39	52.0	1493	2	O9H4G2_HUMAN	O9H4G2 homo sapien
72	39	52.0	1502	2	O9ULI8_HUMAN	O9ULI8 homo sapien
73	38.5	51.3	185	2	O80G66_9POXY	O80G66 orf vlrus s
74	38.5	51.3	611	2	O9X582_STRLA	O9X582 streptomyces
75	38	50.7	73	2	O8TXL6_METRA	O8TXL6 methanopyru
76	38	50.7	101	2	O86J32_MYCTU	O86J32 mycobacteri
77	38	50.7	101	2	O7U1Y4_MYCBO	O7U1Y4 mycobacteri
78	38	50.7	128	2	O8N4Y0_HUMAN	O8N4Y0 homo sapien
79	38	50.7	157	2	O4LH64_9BURK	O4LH64 burkholderi
80	38	50.7	174	2	P72803_SYNY3	P72803 synechocyst
81	38	50.7	186	1	ATG12_YEAST	P81316 aschacharomyc
82	38	50.7	197	2	O5RJS0_RAT	O5RJS0 rattus norv
83	38	50.7	250	2	O93L06_BURPS	O93L06 burkholderi
84	38	50.7	259	2	O90572_GINCI	O90572 gingiymasto
85	38	50.7	297	2	O7K405_TRICA	O7K405 tribolium c
86	38	50.7	302	2	O9ATD5_GOSHI	O9ATD5 goseypium h
87	38	50.7	309	1	XERD_BRUAB	O9FDD0 bruceella ab
88	38	50.7	324	2	O9AWL1_ORYSA	O9AWL1 oryza sativ
89	38	50.7	351	2	O9IXT1_RAT	O9IXT1 rattus norv
90	38	50.7	359	1	AROC_MANSU	O65U87 manneimela
91	38	50.7	367	2	O4LST3_9BURK	O4LST3 burkholderi
92	38	50.7	390	2	O8KTR5_CANTP	O8KTR5 candidatus
93	38	50.7	392	2	O92B53_9BURK	O92B53 candidatus
94	38	50.7	394	2	O9F501_CCTVA	O9F501 etichloro
95	38	50.7	394	2	O6NDB6_RHOBA	O6NDB6 rhodospirito
96	38	50.7	405	2	O86BF2_DROME	O86BF2 drosophila
97	38	50.7	439	2	O41757_MAIZE	O41757 zea mays (m
98	38	50.7	445	2	O6FZD9_SOLDP	O6FZD9 solanum dem
99	38	50.7	447	2	O87LD6_VIBRA	O87LD6 vibrio para
100	38	50.7	473	2	O7NGS0_GLOVY	O7NGS0 geobacter
101	38	50.7	513	2	O5H282_XENLA	O5H282 xenopus lae
102	38	50.7	567	2	O9SKG0_ARATH	O9SKG0 arabidopsis
103	38	50.7	670	2	O70653_GALV	O70653 gibbon ape
104	38	50.7	670	2	O9YWM0_GALV	O9YWM0 gibbon ape

105	38	50.7	752	2	Q4WKC8	ASPFU	Q4kcb	aspergillus
106	38	50.7	785	2	Q8BNG6	MOUSE	Q8bng6	mus musculus
107	38	50.7	846	2	Q584Y3	GYRYP	Q584y3	trypanosoma
108	38	50.7	851	2	Q4WE57	ASPFU	Q4we57	aspergillus
109	38	50.7	935	2	Q5U4H2	MOUSE	Q5u4h2	mus musculus
110	38	50.7	1089	2	Q7Q135	ANOGA	Q7q135	anopheles g
111	38	50.7	1473	2	Q54TV0	DICDI	Q54tv0	dictyostell
112	38	50.7	1589	2	Q6QOV9	MOUSE	Q6qov9	mus musculus
113	38	50.7	2204	2	Q7TTP5	9ENTO	Q7tpp5	human coxsa
114	38	50.7	2381	2	Q5TNW6	ANOGA	Q5tnw9	anopheles g
115	38	50.7	2414	1	EP300	HUMAN	Q09472	homo sapien
116	38	50.7	2414	1	Q5W1B6	HUMAN	Q5w1b6	mus musculi
117	38	50.7	2429	2	Q8QZV8	MOUSE	Q8qzv8	mus musculi
118	38	50.7	2441	1	CBP	MOUSE	P45481	mus musculi
119	38	50.7	2442	1	Q6JHJ9	RAT	Q6jhu9	rattus norv
120	37.5	50.0	131	2	Q5C662	SCHJA	Q5c662	schistosoma
121	37.5	50.0	392	2	Q8ZM97	SATYA	Q8zm97	batimomella
122	37.5	50.0	392	2	Q5PEP2	SALPA	Q5pep2	batimomella
123	37.5	50.0	698	2	Q5HJD3	STAAC	Q5hjd3	staphylococ
124	37.5	50.0	698	2	Q7A7W0	STAMN	Q7a7w0	staphylococ
125	37.5	50.0	698	2	Q8NY12	STAMN	Q8ny12	staphylococ
126	37.5	50.0	698	2	Q99WX9	STAMN	Q99wx9	staphylococ
127	37.5	50.0	705	2	Q6GCN0	STMAS	Q6gcno	staphylococ
128	37	49.3	76	2	Q4KB77	PSEF5	Q4kb77	pseudomonas
129	37	49.3	133	2	Q9M9Q8	ARATX	Q9mq98	pseudomonas
130	37	49.3	138	2	Q05549	LISMO	Q05549	atrididopsis
131	37	49.3	140	2	Q95SC6	DROME	Q95sc6	listeria mo
132	37	49.3	161	2	Q63KK1	BURPS	Q63kk1	burkholderi
133	37	49.3	161	2	Q6ZC14	BURMA	Q6zc14	burkholderi
134	37	49.3	187	2	Q7XJ03	ORYSA	Q7xj03	oryza sativ
135	37	49.3	200	2	Q7MU67	PORGI	Q7mu67	porphyromon
136	37	49.3	217	2	Q55KG7	CRYNE	Q55kg7	cryptococcu
137	37	49.3	217	2	Q5K941	CRYNE	Q5k941	cryptococcu
138	37	49.3	227	2	P95471	PSEBL	P95471	pseudomonas
139	37	49.3	227	2	Q4ZP22	PSEBY	Q4zp22	pseudomonas
140	37	49.3	227	2	Q93SN1	PSEBU	Q93sn1	pseudomonas
141	37	49.3	227	2	Q4K766	PSEF5	Q4k766	pseudomonas
142	37	49.3	227	2	Q87X16	PSEBM	Q87x16	pseudomonas
143	37	49.3	227	2	Q88PE9	PSEBPX	Q88pe9	pseudomonas
144	37	49.3	234	2	Q8MKV1	DROME	Q8mkv1	drosophila
145	37	49.3	236	2	Q416K4	GIBZE	Q416k4	gibberella
146	37	49.3	245	2	P91668	DROME	P91668	drosophila
147	37	49.3	245	2	Q94536	DROME	Q94536	drosophila
148	37	49.3	259	2	Q8G5H4	BIFLO	Q8g5h4	bifidobacte
149	37	49.3	271	2	Q5OEC6	STREFL	Q5oec6	streptomyce
150	37	49.3	279	2	Q4NHT8	9MTC	Q4nht8	arthrobacte
151	37	49.3	282	2	Q93ME7	AMTMD	Q93me7	amycolatops
152	37	49.3	283	2	Q5LE14	BACFN	Q5le14	bacteroides
153	37	49.3	283	2	Q64V51	BACFR	Q64v51	bacteroides
154	37	49.3	318	2	Q6BFX6	PARTB	Q6bfx6	parametium
155	37	49.3	338	2	Q4HXY9	GIBZE	Q4hxy9	gibberella
156	37	49.3	360	1	AROC	VERPE	Q8zd41	vervaina pe
157	37	49.3	361	1	AROC	ERWCT	Q6ddm6	eryvaina car
158	37	49.3	361	1	AROC	YERPS	Q668v5	yeraina ps
159	37	49.3	366	1	AROC	CHRVO	Q7nytc	chromobacte
160	37	49.3	366	1	AROC	RALSO	Q8xz40	talastonia s
161	37	49.3	366	1	Q4L1F3	9BURK	Q4l1f3	burkholderi
162	37	49.3	369	1	AROC	BTRMA	Q6zku7	burkholderi
163	37	49.3	369	1	AROC	BURPS	Q63tk6	burkholderi
164	37	49.3	377	1	AROC	AROSE	Q5pik1	azotarcus sp
165	37	49.3	381	2	Q6K307	ORYSA	Q6k307	oryza sativ
166	37	49.3	383	2	Q6G9S9	STMAS	Q6g9s9	staphylococ
167	37	49.3	383	2	Q6GHF1	STARS	Q6ghf1	staphylococ
168	37	49.3	383	2	Q5HGE7	STAAC	Q5hge7	staphylococ
169	37	49.3	383	2	Q7ASW9	STAMN	Q7asw9	staphylococ
170	37	49.3	383	2	Q8NMY3	STAMN	Q8nmy3	staphylococ
171	37	49.3	383	2	Q99UI8	STAMN	Q99ui8	oryza sativ
172	37	49.3	385	2	Q6K306	ORYSA	Q6k306	oryza sativ
173	37	49.3	392	2	Q9ZG19	9BURK	Q9zgi9	alcaligenes
174	37	49.3	393	2	Q4LM20	9BURK	Q4lm20	burkholderi
175	37	49.3	393	2	Q4LPE9	9BURK	Q4lpe9	burkholderi
176	37	49.3	404	2	Q64BM8	9ARCH	Q64bm8	uncultured
177	37	49.3	407	2	Q5BRP6	RHIME	Q5brp6	rhizobium m
178	37	49.3	414	2	Q7SGE9	NEUCR	Q7sge9	neurospora
179	37	49.3	423	2	Q67SG8	SYMTH	Q67sg8	symbiobacte
180	37	49.3	426	2	Q4GZB6	GYRYP	Q4gzb6	trypanosoma
181	37	49.3	443	1	COX10	MOUSE	COX10	mus musculi
182	37	49.3	447	2	Q8DE97	VIBVU	Q8de97	vibrio vuln
183	37	49.3	447	2	Q7MPC3	VIBVY	Q7mpc3	vibrio vuln
184	37	49.3	451	2	Q35390	RAT	Q35390	rattus norv
185	37	49.3	467	2	Q7QGL5	ANOGA	Q7qgl5	anopheles g
186	37	49.3	475	2	Q7XBS1	ORYSA	Q7xbs1	oryza sativ
187	37	49.3	475	2	Q9FRN5	ORYSA	Q9frn5	oryza sativ
188	37	49.3	515	2	Q7Y2B4	BPR69	Q7y2b4	bacterioph
189	37	49.3	519	2	Q4HYN0	GIBZE	Q4hyn0	gibberella
190	37	49.3	529	2	Q5GUD7	XANOR	Q5gud7	xanthomonas
191	37	49.3	534	2	Q7L527	HUMAN	Q7l527	homo sapien
192	37	49.3	548	2	Q61CS6	CAEBR	Q61cs6	caenorhabdi
193	37	49.3	552	2	Q8WU59	HUMAN	Q8wu59	homo sapien
194	37	49.3	553	2	Q94DS2	ORYSA	Q94ds2	oryza sativ
195	37	49.3	561	2	Q4Q127	LEIMA	Q4q127	leishmania
196	37	49.3	575	2	Q55ZM8	CRYNE	Q55zm8	cryptococcu
197	37	49.3	591	2	Q8C8V4	MOUSE	Q8c8v4	mus musculi
198	37	49.3	595	2	Q5JRW7	HUMAN	Q5jrw7	homo sapien
199	37	49.3	630	2	Q5VSI1	BRARE	Q5vsi1	brachydantio
200	37	49.3	631	2	Q8SVR8	DROME	Q8svr8	drosophila
201	37	49.3	631	2	Q9VZD7	DROME	Q9vzd7	drosophila
202	37	49.3	636	2	Q9UPP8	HUMAN	Q9upp8	homo sapien
203	37	49.3	637	2	Q4W8R3	HORVU	Q4w8r3	hordeum vul
204	37	49.3	638	2	Q52VR0	WHEAT	Q52vr0	triticeum ae
205	37	49.3	647	2	Q8PX77	MEYMA	Q8px77	methanosarc
206	37	49.3	665	1	GAB2	MOUSE	Q9t1a8	mus musculi
207	37	49.3	665	1	GAB2	RAT	Q9eqh1	rattus norv
208	37	49.3	666	2	Q7XWU2	ORYSA	Q7xwu2	oryza sativ
209	37	49.3	667	2	Q61FL2	CAEBR	Q61fl2	caenorhabdi
210	37	49.3	667	2	Q19201	CABEL	Q19201	caenorhabdi
211	37	49.3	676	1	GAB2	HUMAN	Q9yuc2	homo sapien
212	37	49.3	697	2	Q5H3A7	XANOR	Q5h3a7	xanthomonas
213	37	49.3	702	2	Q61JG8	CAEBR	Q61jg8	caenorhabdi
214	37	49.3	732	2	Q5EMU6	CRYNE	Q5emu6	cryptococcu
215	37	49.3	732	2	Q5KB73	CRYNE	Q5kb73	cryptococcu
216	37	49.3	738	2	Q9N615	LEIMA	Q9n615	leishmania
217	37	49.3	744	2	Q65D63	BACLD	Q65d63	bacillus ll
218	37	49.3	853	2	Q9H8M5	HUMAN	Q9h8m5	homo sapien
219	37	49.3	854	2	Q5T569	HUMAN	Q5t569	homo sapien
220	37	49.3	875	2	Q5U2P1	RAT	Q5u2p1	rattus norv
221	37	49.3	876	2	Q5T570	HUMAN	Q5t570	homo sapien
222	37	49.3	886	2	Q9VM64	DROME	Q9vm64	drosophila
223	37	49.3	899	2	Q98TDO	CHICK	Q98tdo	gallus gall
224	37	49.3	962	2	Q825B5	STRAW	Q825b5	streptomyce
225	37	49.3	1022	2	Q4S3R8	TETNG	Q4s3r8	tetradodon n
226	37	49.3	1037	2	Q9BS16	HUMAN	Q9bs16	homo sapien
227	37	49.3	1037	2	Q5JRX3	HUMAN	Q5jrx3	homo sapien
228	37	49.3	1037	2	Q4VBR1	HUMAN	Q4vbr1	homo sapien
229	37	49.3	1037	2	Q5RDX3	PONPY	Q5rdx3	pongo pygma
230	37	49.3	1038	2	Q952D4	HUMAN	Q952d4	homo sapien
231	37	49.3	1052	2	Q23424	ARATH	Q23424	arabidopsis
232	37	49.3	1059	2	Q8G9Y1	ARATH	Q8g9y1	arabidopsis
233	37	49.3	1061	2	Q7U9J3	SYNPK	Q7u9j3	synechococc
234	37	49.3	1074	2	Q4NPD9	9DELT	Q4npd9	anaeromyxob
235	37	49.3	1106	2	Q9YH35	TETFL	Q9yh35	tetradodon f
236	37	49.3	1256	2	Q9M297	ARATH	Q9m297	arabidopsis
237	37	49.3	1395	2	Q6JB16	RAT	Q6jb16	rattus norv
238	37	49.3	1437	2	Q4P0S7	USTMA	Q4p0s7	ustillago ma
239	37	49.3	1609	2	Q5CXK9	CRYPV	Q5cxk9	cryptospori
240	37	49.3	1729	2	Q6JB17	RAT	Q6jb17	rattus norv
241	37	49.3	1744	2	Q4PE16	USTMA	Q4pe16	ustillago ma
242	37	49.3	1900	2	Q7SDP9	NEUCR	Q7sdp9	neurospora
243	37	49.3	1999	2	Q4YAG7	PLABE	Q4yag7	plasmodium
244	37	49.3	2072	2	Q4SA09	TETNG	Q4sa09	tetradodon n
245	37	49.3	2396	2	Q7U132	RHOBA	Q7u132	rhodospirell
246	37	49.3	2713	2	Q6D9L1	ERWCT	Q6d9l1	eryvaina car
247	36.5	48.7	393	1	YOBF	ECOLI	Q46939	escherichia
248	36.5	48.7	394	2	Q8RE66	ECOL6	Q8re66	escherichia
249	36.5	48.7	394	2	Q8X617	ECOS7	Q8x617	escherichia
250	36.5	48.7	497	2	Q746K5	THET2	Q746k5	thermus the

251	36.5	48.7	497	2	053w69	THE8	053w69	thermus the	324	36	48.0	525	2	08L372	ORYSA	08L372	oryza sativ
252	36.5	48.7	716	2	04Q391	LEIMA	04Q391	leishmania	325	36	48.0	530	2	04MM21	ASPFU	04MM21	aspeygiilus
253	36.5	48.7	970	2	07RXPT	NEUPC	07RXPT	neuropora	326	36	48.0	543	2	082SM0	NITRU	082SM0	nitrosomonas
254	36	48.0	62	2	041571	WHEAT	041571	trititum ae	327	36	48.0	549	2	041HY0	GIBZE	041HY0	gibberella
255	36	48.0	87	2	04TG48	TETNG	04TG48	tetrarodon n	328	36	48.0	550	2	0743G4	MYCPA	0743G4	mycobacteri
256	36	48.0	96	2	08B8T9	PSESM	08B8T9	pseudomonas	329	36	48.0	551	2	093H30	STRAW	093H30	strepptomyc
257	36	48.0	119	2	074A28	GEOSTL	074A28	geobacter s	330	36	48.0	568	2	04PAU2	USTMA	04PAU2	ustiliago ma
258	36	48.0	153	2	0930P2	RHIME	0930P2	rhizobium m	331	36	48.0	578	2	055PFO	CRVNE	055PFO	cryptococcu
259	36	48.0	155	2	07UGT7	RHOHA	07UGT7	rhodospirell	332	36	48.0	580	2	089RH2	BRAYA	089RH2	bradyrhizob
260	36	48.0	177	2	06USZ8	9SMEG	06USZ8	syngnathus	333	36	48.0	582	2	05KEB8	CRVNE	05KEB8	cryptococcu
261	36	48.0	181	2	091TT4	TUHV1	091TT4	cupatid her	334	36	48.0	585	2	041404	GIBZE	041404	gibberella
262	36	48.0	192	1	Y4LH	RHISN	P55548	rhizobium s	335	36	48.0	595	2	057U00	9TRYP	057U00	trypanosoma
263	36	48.0	206	2	087CQ7	XYLFT	087CQ7	xyliella fas	336	36	48.0	610	2	05YQ15	NOCFA	05YQ15	nocardia fa
264	36	48.0	226	2	07PL26	DROME	07PL26	pseudomonas	337	36	48.0	625	1	THIC	XANAC	06CUD5	kluyveromyc
265	36	48.0	227	2	09HW21	PSEAE	09HW21	pseudomonas	338	36	48.0	648	2	06CUD5	KLUJA	06CUD5	kluyveromyc
266	36	48.0	236	2	04YE08	PLABE	04YE08	plamedium	339	36	48.0	659	2	052FY4	MAGGR	052FY4	magnaporthe
267	36	48.0	242	2	09FAY9	BACHD	09FAY9	bacillus ha	340	36	48.0	661	2	04P7X4	USTMA	04P7X4	ustiliago ma
268	36	48.0	244	2	08ELB2	OCEIH	08ELB2	oceanobacil	341	36	48.0	662	1	UL06	HHV6U	0785M3	9BETA
269	36	48.0	248	2	04HSF1	9DEIO	04HSF1	deinococcus	342	36	48.0	662	1	UL06	HHV6U	0785M3	9BETA
270	36	48.0	254	2	09KZD4	STRCO	09KZD4	strepptomyc	343	36	48.0	662	2	0785M3	9BETA	0785M3	9BETA
271	36	48.0	268	2	09APU3	PSEAE	09APU3	pseudomonas	344	36	48.0	662	2	057138	9BETA	057138	9BETA
272	36	48.0	276	2	07NU01	CHRV0	07NU01	chromobacte	345	36	48.0	687	2	04T017	TETNG	04T017	TETNG
273	36	48.0	287	2	06CE60	YARLI	06CE60	yarowia li	346	36	48.0	717	2	05NPM4	ZYMOC	05NPM4	zymomonas m
274	36	48.0	297	2	09W2B4	DROME	09W2B4	tetrarodon n	347	36	48.0	727	2	05H4R6	XANOR	05H4R6	xanthomonas
275	36	48.0	300	2	04THH6	TETNG	04THH6	tetrarodon n	348	36	48.0	738	2	07S415	NEUCR	07S415	neurospora
276	36	48.0	312	2	05XHE2	PHACH	05XHE2	phanerocha	349	36	48.0	739	2	04SAG9	TETNG	04SAG9	tetraspora
277	36	48.0	312	2	0516G3	CHLAB	0516G3	chlamydomophi	350	36	48.0	755	2	0524I8	MAGGR	0524I8	magnaporthe
278	36	48.0	312	2	0823T9	CHLCV	0823T9	chlamydomophi	351	36	48.0	763	2	0747H4	GEOSTL	0747H4	geobacter s
279	36	48.0	315	1	XERC	CHLMU	09KH47	phlanerydia m	352	36	48.0	766	2	04P734	USTMA	04P734	ustiliago ma
280	36	48.0	315	2	05XHE3	PHACH	05XHE3	phanerocha	353	36	48.0	849	2	019070	CAEEL	019070	caenorhabdi
281	36	48.0	315	2	05XHE5	PHACH	05XHE5	phanerocha	354	36	48.0	880	2	0583Q4	9TRYP	0583Q4	trypanosoma
282	36	48.0	315	2	04NEC0	9MICC	04NEC0	athrobacte	355	36	48.0	882	2	05AXO8	EMENI	05AXO8	aspergillus
283	36	48.0	319	2	05LSV2	STLPO	05LSV2	silicibacte	356	36	48.0	925	2	025342	LEIMA	025342	leishmania
284	36	48.0	331	2	09R6M4	9RHIZ	09R6M4	agrobacteri	357	36	48.0	948	2	04GZD5	9TRYP	04GZD5	trypanosoma
285	36	48.0	333	2	08KGP6	RHIL0	08KGP6	rhizobium l	358	36	48.0	974	2	023463	CAEEL	023463	caenorhabdi
286	36	48.0	338	1	6PGL	CANBP	07VR18	canididatus	359	36	48.0	975	2	061194	CAEHR	061194	caenorhabdi
287	36	48.0	343	2	09SVJ6	ARATH	09SVJ6	arabidopsis	360	36	48.0	1037	2	081S18	DICDI	081S18	dictyostelli
288	36	48.0	344	2	09WDB1	9INFB	09WDB1	influenza b	361	36	48.0	1083	2	07SB63	NEUCR	07SB63	neuropora
289	36	48.0	353	1	AROC	BORRA	07RKJ5	borderella	362	36	48.0	1110	2	07PPP4	ANOGA	07PPP4	anopheles g
290	36	48.0	353	1	AROC	BORRA	07W950	borderella	363	36	48.0	1144	2	06FLT9	CANGA	06FLT9	cangia
291	36	48.0	353	1	AROC	BORPE	07VY92	borderella	364	36	48.0	1173	2	P92199	CAEEL	P92199	caenorhabdi
292	36	48.0	356	2	08Y230	RALSO	07VRUC	ralstonia s	365	36	48.0	1196	2	04RNS0	TETNG	04RNS0	tetraspora
293	36	48.0	357	1	AROC	CANBP	061J96	canididatus	366	36	48.0	1208	2	06FSL9	CANGA	06FSL9	cangia
294	36	48.0	382	2	061J96	CAEHR	061J96	caenorhabdi	367	36	48.0	1226	2	08TKX2	DROME	08TKX2	drosophila
295	36	48.0	393	2	08R8U5	LEPIN	08R8U5	leptosira	368	36	48.0	1226	2	09VX92	DROME	09VX92	drosophila
296	36	48.0	393	2	07ZV45	LEPIC	07ZV45	leptosira	369	36	48.0	1284	2	09WJ35	9VIRU	09WJ35	salmon panc
297	36	48.0	393	2	06U504	BRARE	06U504	brachydano	370	36	48.0	1320	2	08JUX0	9VIRU	08JUX0	salmon panc
298	36	48.0	395	2	0577S7	BRUAB	0577S7	bruceella ab	371	36	48.0	1330	2	09SXQ2	ARATH	09SXQ2	arabidopsis
299	36	48.0	397	2	04K6J8	PSEFS	04K6J8	pseudomonas	372	36	48.0	1364	2	05AGZ6	CANAL	05AGZ6	candida alb
300	36	48.0	398	2	05XER6	ARATH	05XER6	arabidopsis	373	36	48.0	1431	2	09SXQ1	ARATH	09SXQ1	arabidopsis
301	36	48.0	398	2	0944G9	ARATH	0944G9	arabidopsis	374	36	48.0	1442	2	07SEB7	NEUCR	07SEB7	neuropora
302	36	48.0	407	2	061VW0	BRARE	061VW0	brachydano	375	36	48.0	1447	2	09SXQ3	ARATH	09SXQ3	arabidopsis
303	36	48.0	407	2	056H80	BRARE	056H80	brachydano	376	36	48.0	1456	2	09ZT94	ARATH	09ZT94	arabidopsis
304	36	48.0	407	2	0502T5	BRARE	0502T5	brachydano	377	36	48.0	1460	2	06BUJ9	DEBHA	06BUJ9	debaromyce
305	36	48.0	409	2	041Z68	AZOV1	041Z68	azobacter	378	36	48.0	1466	2	04HMW2	ARATH	04HMW2	arabidopsis
306	36	48.0	410	2	08RWD1	BRUSU	08RWD1	bruceella su	379	36	48.0	1466	2	094HW7	ARATH	094HW7	arabidopsis
307	36	48.0	410	2	08BYB6	BRUME	08BYB6	bruceella me	380	36	48.0	1475	2	09SXQ4	ARATH	09SXQ4	arabidopsis
308	36	48.0	424	2	018207	CABEL	018207	caenorhabdi	381	36	48.0	1518	2	06CER0	YARLI	06CER0	yarowia li
309	36	48.0	430	2	06FJ25	CANGA	06FJ25	candida gla	382	36	48.0	1600	2	04RTT2	TETNG	04RTT2	tetraspora
310	36	48.0	430	2	0852K2	ORYSA	0852K2	oryza sativ	383	36	48.0	1647	2	04P2M4	USTMA	04P2M4	ustiliago ma
311	36	48.0	434	2	04LPR5	9BURK	04LPR5	burkholderi	384	36	48.0	1681	2	04SVT8	TETNG	04SVT8	tetraspora
312	36	48.0	440	2	089C12	BRAYA	089C12	bradyrhizob	385	36	48.0	1774	2	04IKH0	GIBZE	04IKH0	gibberella
313	36	48.0	447	2	09KPP4	VTBCH	09KPP4	vibrio chol	386	36	48.0	1829	2	093Y68	ORYSA	093Y68	oryza sativ
314	36	48.0	456	2	0701Z5	9STRA	0701Z5	botrydiodipsi	387	36	48.0	1845	2	057MA9	9TRYP	057MA9	trypanosoma
315	36	48.0	460	2	05E7H3	VIBF1	05E7H3	vibriol fisc	388	36	48.0	2190	2	04HZZ0	9TRYP	04HZZ0	trypanosoma
316	36	48.0	468	2	098C98	RHIL0	098C98	rhizobium l	389	36	48.0	2503	2	057ZV0	9TRYP	057ZV0	trypanosoma
317	36	48.0	469	2	08G604	BIFLO	08G604	bifidobacte	390	36	47.3	338	2	09D1U9	MOUSE	09D1U9	mus musculu
318	36	48.0	473	2	06GPP3	ORYSA	06GPP3	oryza sativ	391	35.5	47.3	338	2	0981L1	RHIL0	0981L1	rhizobium l
319	36	48.0	476	2	083632	TREPA	083632	treponema p	392	35.5	47.3	392	2	087H42	YIBPA	087H42	vibrio para
320	36	48.0	479	2	07ZEP9	DESVH	07ZEP9	desulfatovibr	393	35.5	47.3	396	2	0410D7	GIBZE	0410D7	gibberella
321	36	48.0	479	2	04PAP7	USTMA	04PAP7	ustiliago ma	394	35.5	47.3	396	2	04KCE1	PSEFS	04KCE1	pseudomonas
322	36	48.0	516	2	04SMLO	TETNG	04SMLO	tetrarodon n	395	35.5	47.3	402	2	04ZS07	PSEFS	04ZS07	pseudomonas
323	36	48.0	524	2	06QZHE	DROYA	06QZHE	drosophila	396	35.5	47.3	402	2	0880J3	PSEFS	0880J3	pseudomonas

397	35.5	47.3	440	2	Q9KSD9_VIBCH	Q9ked9 vibrio chol	470	35	46.7	236	2	Q4LQZ4_9BURK	Q4lqz4 burkholderi
398	35.5	47.3	790	2	Q9SB53_ARATH	Q9sb53 arabidopsis	471	35	46.7	236	2	Q88G03_PSEPK	Q88g03 pseudomonas
399	35.5	47.3	12925	2	Q4Q10_LEIMA	Q4q10 leishmania	472	35	46.7	238	2	Q22600_CAEEL	Q22600 caenorhabdi
400	35	46.7	65	2	Q8UZLO_9VIRU	Q8uzlo salmon panc	473	35	46.7	240	2	Q91CP9_9INFB	Q91cp9 influenza b
401	35	46.7	75	2	Q6SKF1_APTAU	Q6skf1 arthropace	474	35	46.7	240	2	Q50DB1_9INFB	Q50db1 influenza b
402	35	46.7	79	2	Q8T602_PLAF7	Q8t602 plasmodium	475	35	46.7	240	2	Q50DB2_9INFB	Q50db2 influenza b
403	35	46.7	90	2	Q8CAG1_MOUSE	Q8cag1 mus musculi	476	35	46.7	242	2	Q50DB1_9INFB	Q50db1 influenza b
404	35	46.7	92	2	Q5RHY5_BRARE	Q5rhy5 brachydanio	477	35	46.7	242	2	Q50DB5_9INFB	Q50db5 influenza b
405	35	46.7	96	2	Q5Q0H9_ARATH	Q5qoh9 arabidopsis	478	35	46.7	243	2	Q6U812_9INFB	Q6u812 influenza b
406	35	46.7	110	2	Q9HBX3_HUMAN	Q9hbx3 homo sapien	479	35	46.7	243	2	Q91CQ0_9INFB	Q91cq0 influenza b
407	35	46.7	115	2	Q6CP00_KILTA	Q6cp00 klyveromyc	480	35	46.7	243	2	Q50DA7_9INFB	Q50da7 influenza b
408	35	46.7	128	2	Q5Q010_ARATH	Q5qio10 arabidopsis	481	35	46.7	245	2	Q6U8F7_9INFB	Q6u8f7 influenza b
409	35	46.7	131	2	Q8T540_PLAFA	Q8t540 plasmodium	482	35	46.7	246	2	Q6U8F6_9INFB	Q6u8f6 influenza b
410	35	46.7	134	2	Q8T529_PLAFA	Q8t529 plasmodium	483	35	46.7	246	2	Q6U815_9INFB	Q6u815 influenza b
411	35	46.7	137	2	Q9RT41_DEIRA	Q9rt41 deinococcus	484	35	46.7	257	2	Q75173_9INFB	Q75173 influenza b
412	35	46.7	139	2	Q4T0J1_TETNG	Q4tj1 tetradon n	485	35	46.7	262	2	Q8CPFS_STAEP	Q8cpfs ectopyletic
413	35	46.7	142	2	Q5R0J0_EMENT	Q5r0j0 aspergillus	486	35	46.7	262	2	Q8NQ08_CORGL	Q8nq08 corynebacte
414	35	46.7	145	2	Q6J1F2_MACRS	Q6j1f2 macrobrachi	487	35	46.7	267	1	TRBJ_RHISN	Trbj rhizobium s
415	35	46.7	156	2	Q53QY2_HUMAN	Q53gy2 homo saplen	488	35	46.7	283	2	Q6MBG9_PARUV	Q6mbg9 parachlamy
416	35	46.7	162	1	RECX_XANCP	Q8p9x1 xanthomonas	489	35	46.7	289	2	Q4T6X8_TETNG	Q4t6x8 tetradon n
417	35	46.7	162	2	Q4UTR5_XANCP	Q4utr5 xanthomonas	490	35	46.7	291	2	Q691X3_ORYSA	Q691x3 oryza sativ
418	35	46.7	163	2	Q6KAN5_MOUSE	Q6kan5 mus musculi	491	35	46.7	292	2	Q4RZES_TETNG	Q4rzes tetradon n
419	35	46.7	169	2	Q6AN69_DESPS	Q6an69 desulfofate	492	35	46.7	295	2	Q9HAD3_HUMAN	Q9had3 homo sapien
420	35	46.7	174	2	Q7D3T2_AGRFS	Q7d3t2 agrobacteri	493	35	46.7	295	2	Q4Q1T4_LEIMA	Q4q1t4 leishmania
421	35	46.7	175	2	PANH_ECOLI	P20b62 escherichia	494	35	46.7	296	2	Q5SCC1_OSTTA	Q5scc1 ostrea
422	35	46.7	176	2	Q4H506_9DBIO	Q4h506 deinococcus	495	35	46.7	297	1	XERD_PASMU	Xerd pasmu
423	35	46.7	178	2	Q97SY3_STREP	Q97sy3 streptococc	496	35	46.7	298	2	Q65UK7_MANSM	Q65uk7 mansm
424	35	46.7	182	2	Q9FRCO_ORYSA	Q9fc9 oryza sativ	497	35	46.7	298	2	Q5ZG64_9INFB	Q5zg64 influenza b
425	35	46.7	187	2	Q8CWM9_STPR6	Q8cwm9 streptococc	498	35	46.7	298	2	Q4LCR3_9INFB	Q4lcr3 influenza b
426	35	46.7	188	2	Q5AAM4_CANAL	Q5aam4 candida alb	499	35	46.7	299	2	Q9BKZ7_RHILLO	Q9bkz7 rhizobium l
427	35	46.7	191	2	Q5YFM5_9VIRU	Q5yfm5 singapore g	500	35	46.7	300	1	XERC_MYXXA	Xerc myxxa
428	35	46.7	194	2	Q8MW87_9TURB	Q8mw87 thysanozoon	501	35	46.7	306	2	Q7V592_PROMM	Q7v592 prochlorococ
429	35	46.7	200	2	Q5ODP6_9INFB	Q5odf6 influenza b	502	35	46.7	308	2	Q8JP44_9INFB	Q8jp44 influenza b
430	35	46.7	203	2	Q8MW92_DUGTI	Q8mw92 dugesia tlg	503	35	46.7	309	1	XERD_BRUME	Xerd bruceella me
431	35	46.7	204	2	Q8MW88_9TURB	Q8mw88 discoceclie	504	35	46.7	309	1	XERD_BRUSU	Xerd brusula su
432	35	46.7	204	2	Q5ODH4_9INFB	Q5odh4 influenza b	505	35	46.7	311	2	Q4ICS2_9INFB	Q4ics2 influenza b
433	35	46.7	206	2	Q4FQV1_9GAMM	Q4fqv1 psychrobact	506	35	46.7	317	2	Q6CAB9_YARLI	Q6cab9 yarrowia li
434	35	46.7	208	2	Q5ODD1_9INFB	Q5odd1 influenza b	507	35	46.7	318	2	Q801Y7_9INFB	Q801y7 influenza b
435	35	46.7	211	2	Q5ODP9_9INFB	Q5odf9 influenza b	508	35	46.7	318	2	Q801Y8_9INFB	Q801y8 influenza b
436	35	46.7	211	2	Q5ODG7_9INFB	Q5odg7 influenza b	509	35	46.7	318	2	Q801Y9_9INFB	Q801y9 influenza b
437	35	46.7	212	2	Q5ODD0_9INFB	Q5odd0 influenza b	510	35	46.7	318	2	Q801Z0_9INFB	Q801z0 influenza b
438	35	46.7	212	2	Q5ODD3_9INFB	Q5odd3 influenza b	511	35	46.7	318	2	Q801Z1_9INFB	Q801z1 influenza b
439	35	46.7	212	2	Q5ODD4_9INFB	Q5odd4 influenza b	512	35	46.7	318	2	Q801Z3_9INFB	Q801z3 influenza b
440	35	46.7	212	2	Q5ODD6_9INFB	Q5odd6 influenza b	513	35	46.7	318	2	Q801Z4_9INFB	Q801z4 influenza b
441	35	46.7	212	2	Q5ODE7_9INFB	Q5ode7 influenza b	514	35	46.7	318	2	Q801Z5_9INFB	Q801z5 influenza b
442	35	46.7	212	2	Q5ODP8_9INFB	Q5odp8 influenza b	515	35	46.7	318	2	Q801Z6_9INFB	Q801z6 influenza b
443	35	46.7	212	2	Q5ODG9_9INFB	Q5odg9 influenza b	516	35	46.7	318	2	Q801Z7_9INFB	Q801z7 influenza b
444	35	46.7	213	2	Q5ODB0_9INFB	Q5odb0 influenza b	517	35	46.7	318	2	Q801Z8_9INFB	Q801z8 influenza b
445	35	46.7	213	2	Q5ODG1_9INFB	Q5odg1 influenza b	518	35	46.7	318	2	Q801Z9_9INFB	Q801z9 influenza b
446	35	46.7	213	2	Q5ODG4_9INFB	Q5odg4 influenza b	519	35	46.7	318	2	Q80J00_9INFB	Q80j00 influenza b
447	35	46.7	214	2	Q5ODE3_9INFB	Q5ode3 influenza b	520	35	46.7	318	2	Q80J01_9INFB	Q80j01 influenza b
448	35	46.7	214	2	Q5ODP1_9INFB	Q5odp1 influenza b	521	35	46.7	318	2	Q80J02_9INFB	Q80j02 influenza b
449	35	46.7	214	2	Q5ODP5_9INFB	Q5odp5 influenza b	522	35	46.7	318	2	Q80J03_9INFB	Q80j03 influenza b
450	35	46.7	214	2	Q5ODH6_9INFB	Q5odh6 influenza b	523	35	46.7	318	2	Q80J04_9INFB	Q80j04 influenza b
451	35	46.7	217	2	Q6MA61_PARUV	Q6ma61 parachlamyd	524	35	46.7	318	2	Q80J06_9INFB	Q80j06 influenza b
452	35	46.7	217	2	Q5ODB5_9INFB	Q5odb5 influenza b	525	35	46.7	318	2	Q80J07_9INFB	Q80j07 influenza b
453	35	46.7	217	2	Q5ODE4_9INFB	Q5ode4 influenza b	526	35	46.7	318	2	Q80J08_9INFB	Q80j08 influenza b
454	35	46.7	217	2	Q5ODP7_9INFB	Q5odp7 influenza b	527	35	46.7	318	2	Q80J09_9INFB	Q80j09 influenza b
455	35	46.7	219	2	Q5ODH0_9INFB	Q5odh0 influenza b	528	35	46.7	318	2	Q80J10_9INFB	Q80j10 influenza b
456	35	46.7	219	2	Q91CN5_9INFB	Q91cn5 influenza b	529	35	46.7	318	2	Q80J11_9INFB	Q80j11 influenza b
457	35	46.7	221	2	Q9WXZ2_THEMA	Q9wxz2 thermocoga	530	35	46.7	318	2	Q80QY4_9INFB	Q80qy4 influenza b
458	35	46.7	221	2	Q6U8H9_9INFB	Q6u8h9 influenza b	531	35	46.7	318	2	Q8BVCH_MOUSE	Q8bvch mus musculi
459	35	46.7	222	2	Q9BA52_RHILLO	Q9ba52 rhizobium l	532	35	46.7	321	2	Q5ZG65_9INFB	Q5zg65 influenza b
460	35	46.7	222	2	Q5H2W9_RAT	Q5h2w9 rattus norv	533	35	46.7	322	2	Q6UUP4_ORYSA	Q6uup4 oryza sativ
461	35	46.7	223	1	EVTZA_MOUSE	P20j34 mus musculi	534	35	46.7	323	2	Q5ZG67_9INFB	Q5zg67 influenza b
462	35	46.7	223	2	Q6DKP1_MOUSE	Q6dkp1 m ecotopic	535	35	46.7	325	2	Q8JP55_9INFB	Q8jp55 influenza b
463	35	46.7	223	2	Q5ODH7_9INFB	Q5odh7 influenza b	536	35	46.7	325	2	Q8BAC7_9INFB	Q8bac7 influenza b
464	35	46.7	226	2	Q61EP9_CAEER	Q61ep9 caenorhabdi	537	35	46.7	326	2	Q8BAC8_9INFB	Q8bac8 influenza b
465	35	46.7	227	2	Q61790_CAEEL	Q61790 caenorhabdi	538	35	46.7	326	2	Q8BAC9_9INFB	Q8bac9 influenza b
466	35	46.7	228	2	Q9ANCS_BRJJA	Q9anc3 bradyrhizob	539	35	46.7	326	2	Q8JMP2_9INFB	Q8jmp2 influenza b
467	35	46.7	230	2	Q75T72_9INFB	Q75t72 influenza b	540	35	46.7	326	2	Q8JMP3_9INFB	Q8jmp3 influenza b
468	35	46.7	231	2	Q53P18_ORYSA	Q53p18 oryza sativ	541	35	46.7	326	2	Q8JMP4_9INFB	Q8jmp4 influenza b
469	35	46.7	233	2	Q4ZON3_PLAAB	Q4zon3 plasmodium	542	35	46.7	326	2		

[illegible]

689	35	46.7	345	2	O9YWH2_9INFB	O9Ywh2	influenza b	762	35	46.7	346	2	O77WH8_9INFB	O77wh8	influenza b
690	35	46.7	345	2	O9YWH3_9INFB	O9Ywh3	influenza b	763	35	46.7	346	2	O77WH9_9INFB	O77wh9	influenza b
691	35	46.7	345	2	O9YWH4_9INFB	O9Ywh4	influenza b	764	35	46.7	346	2	O77WH0_9INFB	O77wh0	influenza b
692	35	46.7	345	2	O9YWH5_9INFB	O9Ywh5	influenza b	765	35	46.7	346	2	O77WH1_9INFB	O77wh1	influenza b
693	35	46.7	345	2	O9YWH6_9INFB	O9Ywh6	influenza b	766	35	46.7	346	2	O77WH2_9INFB	O77wh2	influenza b
694	35	46.7	345	2	O9YWH7_9INFB	O9Ywh7	influenza b	767	35	46.7	346	2	O77WH3_9INFB	O77wh3	influenza b
695	35	46.7	345	2	O9YWH8_9INFB	O9Ywh8	influenza b	768	35	46.7	346	2	O77WH4_9INFB	O77wh4	influenza b
696	35	46.7	345	2	O9YWH9_9INFB	O9Ywh9	influenza b	769	35	46.7	346	2	O77WH5_9INFB	O77wh5	influenza b
697	35	46.7	345	2	O9YWH0_9INFB	O9Ywh0	influenza b	770	35	46.7	346	2	O8B924_9INFB	O8B925	influenza b
698	35	46.7	345	2	O9YWH1_9INFB	O9Ywh1	influenza b	771	35	46.7	346	2	O8B925_9INFB	O8B926	influenza b
699	35	46.7	345	2	O9YWH2_9INFB	O9Ywh2	influenza b	772	35	46.7	346	2	O8B928_9INFB	O8B929	influenza b
700	35	46.7	345	2	O9YWH3_9INFB	O9Ywh3	influenza b	773	35	46.7	346	2	O8JP31_9INFB	O8JP32	influenza b
701	35	46.7	345	2	O9YWH4_9INFB	O9Ywh4	influenza b	774	35	46.7	346	2	O8V630_9INFB	O8V630	influenza b
702	35	46.7	345	2	O9YWH5_9INFB	O9Ywh5	influenza b	775	35	46.7	346	2	O911Y6_9INFB	O911Y6	influenza b
703	35	46.7	345	2	O9YWH6_9INFB	O9Ywh6	influenza b	776	35	46.7	346	2	O911Y7_9INFB	O911Y7	influenza b
704	35	46.7	345	2	O9YWH7_9INFB	O9Ywh7	influenza b	777	35	46.7	346	2	O911Y8_9INFB	O911Y8	influenza b
705	35	46.7	345	2	O9YWH8_9INFB	O9Ywh8	influenza b	778	35	46.7	346	2	O911Y9_9INFB	O911Y9	influenza b
706	35	46.7	345	2	O9YWH9_9INFB	O9Ywh9	influenza b	779	35	46.7	346	2	O911Z0_9INFB	O911Z0	influenza b
707	35	46.7	345	2	O9YWH0_9INFB	O9Ywh0	influenza b	780	35	46.7	346	2	O911Z1_9INFB	O911Z1	influenza b
708	35	46.7	345	2	O9YWH1_9INFB	O9Ywh1	influenza b	781	35	46.7	346	2	O911Z2_9INFB	O911Z2	influenza b
709	35	46.7	345	2	O9YWH2_9INFB	O9Ywh2	influenza b	782	35	46.7	346	2	O911Z3_9INFB	O911Z3	influenza b
710	35	46.7	345	2	O9YWH3_9INFB	O9Ywh3	influenza b	783	35	46.7	346	2	O911Z4_9INFB	O911Z4	influenza b
711	35	46.7	345	2	O9YWH4_9INFB	O9Ywh4	influenza b	784	35	46.7	346	2	O911Z5_9INFB	O911Z5	influenza b
712	35	46.7	345	2	O9YWH5_9INFB	O9Ywh5	influenza b	785	35	46.7	346	2	O911Z6_9INFB	O911Z6	influenza b
713	35	46.7	345	2	O9YWH6_9INFB	O9Ywh6	influenza b	786	35	46.7	346	2	O911Z7_9INFB	O911Z7	influenza b
714	35	46.7	345	2	O9YWH7_9INFB	O9Ywh7	influenza b	787	35	46.7	346	2	O911Z8_9INFB	O911Z8	influenza b
715	35	46.7	345	2	O9YWH8_9INFB	O9Ywh8	influenza b	788	35	46.7	346	2	O911Z9_9INFB	O911Z9	influenza b
716	35	46.7	345	2	O4LCQ7_9INFB	O4LCQ7	influenza b	789	35	46.7	346	2	O912A0_9INFB	O912A0	influenza b
717	35	46.7	345	2	O4LCRO_9INFB	O4LCRO	influenza b	790	35	46.7	346	2	O912A1_9INFB	O912A1	influenza b
718	35	46.7	345	2	O4ICSI_9INFB	O4ICSI	influenza b	791	35	46.7	346	2	O912A2_9INFB	O912A2	influenza b
719	35	46.7	345	2	O5XPB6_9INFB	O5XPB6	influenza b	792	35	46.7	346	2	O912A3_9INFB	O912A3	influenza b
720	35	46.7	346	2	O5XPB7_9INFB	O5XPB7	influenza b	793	35	46.7	346	2	O912A4_9INFB	O912A4	influenza b
721	35	46.7	346	2	O5XPB8_9INFB	O5XPB8	influenza b	794	35	46.7	346	2	O91N2_9INFB	O91N2	influenza b
722	35	46.7	346	2	O5XPB9_9INFB	O5XPB9	influenza b	795	35	46.7	346	2	O91NG3_9INFB	O91NG3	influenza b
723	35	46.7	346	2	O5XPC0_9INFB	O5XPC0	influenza b	796	35	46.7	346	2	O91IO4_9INFB	O91IO4	influenza b
724	35	46.7	346	2	O5XPC1_9INFB	O5XPC1	influenza b	797	35	46.7	346	2	O91IO5_9INFB	O91IO5	influenza b
725	35	46.7	346	2	O5XPC2_9INFB	O5XPC2	influenza b	798	35	46.7	346	2	O91IR0_9INFB	O91IR0	influenza b
726	35	46.7	346	2	O5XPC3_9INFB	O5XPC3	influenza b	799	35	46.7	346	2	O9QMS6_9INFB	O9QMS6	influenza b
727	35	46.7	346	2	O6OH70_9INFB	O6OH70	influenza b	800	35	46.7	346	2	O9QWU3_9INFB	O9QWU3	influenza b
728	35	46.7	346	2	O6OH71_9INFB	O6OH71	influenza b	801	35	46.7	346	2	O9QMU4_9INFB	O9QMU4	influenza b
729	35	46.7	346	2	O6OH72_9INFB	O6OH72	influenza b	802	35	46.7	346	2	O9WD49_9INFB	O9WD49	influenza b
730	35	46.7	346	2	O6OH73_9INFB	O6OH73	influenza b	803	35	46.7	346	2	O9WD51_9INFB	O9WD51	influenza b
731	35	46.7	346	2	O6FAN2_9INFB	O6FAN2	influenza b	804	35	46.7	346	2	O9WD52_9INFB	O9WD52	influenza b
732	35	46.7	346	2	O6FAP0_9INFB	O6FAP0	influenza b	805	35	46.7	346	2	O9WD55_9INFB	O9WD55	influenza b
733	35	46.7	346	2	O6FAP3_9INFB	O6FAP3	influenza b	806	35	46.7	346	2	O9WD56_9INFB	O9WD56	influenza b
734	35	46.7	346	2	O6FAP4_9INFB	O6FAP4	influenza b	807	35	46.7	346	2	O9WDAB_9INFB	O9WDAB	influenza b
735	35	46.7	346	2	O6FAP5_9INFB	O6FAP5	influenza b	808	35	46.7	346	2	O9YIP7_9INFB	O9YIP7	influenza b
736	35	46.7	346	2	O6FAP6_9INFB	O6FAP6	influenza b	809	35	46.7	346	2	O9YIS6_9INFB	O9YIS6	influenza b
737	35	46.7	346	2	O6FAP7_9INFB	O6FAP7	influenza b	810	35	46.7	346	2	O9YIT2_9INFB	O9YIT2	influenza b
738	35	46.7	346	2	O6FAP8_9INFB	O6FAP8	influenza b	811	35	46.7	346	2	O9YIV4_9INFB	O9YIV4	influenza b
739	35	46.7	346	2	O6FAP9_9INFB	O6FAP9	influenza b	812	35	46.7	346	2	O9YJCB_9INFB	O9YJCB	influenza b
740	35	46.7	346	2	O6FAQ0_9INFB	O6FAQ0	influenza b	813	35	46.7	346	2	O9YJCB_9INFB	O9YJCB	influenza b
741	35	46.7	346	2	O6FAQ1_9INFB	O6FAQ1	influenza b	814	35	46.7	346	2	O9YJF9_9INFB	O9YJF9	influenza b
742	35	46.7	346	2	O6FAQ2_9INFB	O6FAQ2	influenza b	815	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
743	35	46.7	346	2	O6FAQ3_9INFB	O6FAQ3	influenza b	816	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
744	35	46.7	346	2	O6FAQ4_9INFB	O6FAQ4	influenza b	817	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
745	35	46.7	346	2	O6FAQ5_9INFB	O6FAQ5	influenza b	818	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
746	35	46.7	346	2	O6FAQ6_9INFB	O6FAQ6	influenza b	819	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
747	35	46.7	346	2	O6FAQ7_9INFB	O6FAQ7	influenza b	820	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
748	35	46.7	346	2	O6FAQ8_9INFB	O6FAQ8	influenza b	821	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
749	35	46.7	346	2	O6FAQ9_9INFB	O6FAQ9	influenza b	822	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
750	35	46.7	346	2	O6FAQ0_9INFB	O6FAQ0	influenza b	823	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
751	35	46.7	346	2	O6FAR1_9INFB	O6FAR1	influenza b	824	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
752	35	46.7	346	2	O6FAR2_9INFB	O6FAR2	influenza b	825	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
753	35	46.7	346	2	O71CC2_9INFB	O71CC2	influenza b	826	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
754	35	46.7	346	2	O71CC3_9INFB	O71CC3	influenza b	827	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
755	35	46.7	346	2	O71CC4_9INFB	O71CC4	influenza b	828	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
756	35	46.7	346	2	O77WM2_9INFB	O77WM2	influenza b	829	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
757	35	46.7	346	2	O77WM3_9INFB	O77WM3	influenza b	830	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
758	35	46.7	346	2	O77WM4_9INFB	O77WM4	influenza b	831	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
759	35	46.7	346	2	O77WM5_9INFB	O77WM5	influenza b	832	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
760	35	46.7	346	2	O77WM6_9INFB	O77WM6	influenza b	833	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b
761	35	46.7	346	2	O77WM7_9INFB	O77WM7	influenza b	834	35	46.7	346	2	O9YJG2_9INFB	O9YJG2	influenza b

835	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	908	35	46.7	347	2	O6OH80_9INFB	O6oh80 influenza b
836	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	909	35	46.7	347	2	O6FAP1_9INFB	O6fap1 influenza b
837	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	910	35	46.7	347	2	O6FAP2_9INFB	O6fap2 influenza b
838	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	911	35	46.7	347	2	O7TSV0_9INFB	O7tsv0 influenza b
839	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	912	35	46.7	347	2	O82636_9INFB	O82636 influenza b
840	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	913	35	46.7	347	2	O82637_9INFB	O82637 influenza b
841	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	914	35	46.7	347	2	O82644_9INFB	O82644 influenza b
842	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	915	35	46.7	347	2	O82646_9INFB	O82646 influenza b
843	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	916	35	46.7	347	2	O82649_9INFB	O82649 influenza b
844	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	917	35	46.7	347	2	O82650_9INFB	O82650 influenza b
845	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	918	35	46.7	347	2	O82651_9INFB	O82651 influenza b
846	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	919	35	46.7	347	2	O82654_9INFB	O82654 influenza b
847	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	920	35	46.7	347	2	O82656_9INFB	O82656 influenza b
848	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	921	35	46.7	347	2	O82657_9INFB	O82657 influenza b
849	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	922	35	46.7	347	2	O82658_9INFB	O82658 influenza b
850	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	923	35	46.7	347	2	O82659_9INFB	O82659 influenza b
851	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	924	35	46.7	347	2	O82660_9INFB	O82660 influenza b
852	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	925	35	46.7	347	2	O8B926_9INFB	O8b926 influenza b
853	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	926	35	46.7	347	2	O8B927_9INFB	O8b927 influenza b
854	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	927	35	46.7	347	2	O8B929_9INFB	O8b929 influenza b
855	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	928	35	46.7	347	2	O8JP20_9INFB	O8jp20 influenza b
856	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	929	35	46.7	347	2	O8JP28_9INFB	O8jp28 influenza b
857	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	930	35	46.7	347	2	O8JP31_9INFB	O8jp31 influenza b
858	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	931	35	46.7	347	2	O8JP56_9INFB	O8jp56 influenza b
859	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	932	35	46.7	347	2	O8JP57_9INFB	O8jp57 influenza b
860	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	933	35	46.7	347	2	O8JP59_9INFB	O8jp59 influenza b
861	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	934	35	46.7	347	2	O8V631_9INFB	O8v631 influenza b
862	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	935	35	46.7	347	2	O91NF3_9INFB	O91nf3 influenza b
863	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	936	35	46.7	347	2	O91NF5_9INFB	O91nf5 influenza b
864	35	46.7	346	2	O9WMD_9INFB	O9Wd9 influenza b	937	35	46.7	347	2	O91NF7_9INFB	O91nf7 influenza b
865	35	46.7	347	1	HEMA_INB1	O07925 influenza b	938	35	46.7	347	2	O91NF8_9INFB	O91nf8 influenza b
866	35	46.7	347	1	HEMA_INB2	O07926 influenza b	939	35	46.7	347	2	O91NG1_9INFB	O91ng1 influenza b
867	35	46.7	347	1	HEMA_INB3	O67755 influenza b	940	35	46.7	347	2	O91NG2_9INFB	O91ng2 influenza b
868	35	46.7	347	1	HEMA_INB4	O67756 influenza b	941	35	46.7	347	2	O91F67_9INFB	O91f67 influenza b
869	35	46.7	347	1	HEMA_INB5	O67757 influenza b	942	35	46.7	347	2	O91IQ3_9INFB	O91iq3 influenza b
870	35	46.7	347	1	HEMA_INB6	O67758 influenza b	943	35	46.7	347	2	O9OMS5_9INFB	O9oms5 influenza b
871	35	46.7	347	1	HEMA_INB7	O67759 influenza b	944	35	46.7	347	2	O9OMS7_9INFB	O9oms7 influenza b
872	35	46.7	347	1	HEMA_INB8	O67760 influenza b	945	35	46.7	347	2	O9OMS8_9INFB	O9oms8 influenza b
873	35	46.7	347	1	HEMA_INB9	O07920 influenza b	946	35	46.7	347	2	O9M853_9INFB	O9m853 influenza b
874	35	46.7	347	1	HEMA_INB1B	P18878 influenza b	947	35	46.7	347	2	O9WDS0_9INFB	O9wds0 influenza b
875	35	46.7	347	1	HEMA_INB1A	P18879 influenza b	948	35	46.7	347	2	O9WDS3_9INFB	O9wds3 influenza b
876	35	46.7	347	1	O9FMI_AAVATH	O9fmi1 arebidopeis	949	35	46.7	347	2	O9WDS4_9INFB	O9wds4 influenza b
877	35	46.7	347	2	O9PC4_9INFB	O9pc4 influenza b	950	35	46.7	347	2	O4LCR1_9INFB	O4lcr1 influenza b
878	35	46.7	347	2	O9PC5_9INFB	O9pc5 influenza b	951	35	46.7	347	2	O8JP45_9INFB	O8jp45 influenza b
879	35	46.7	347	2	O9PC6_9INFB	O9pc6 influenza b	952	35	46.7	347	2	O91F65_9INFB	O91f65 influenza b
880	35	46.7	347	2	O9PC7_9INFB	O9pc7 influenza b	953	35	46.7	347	2	O9QAV3_9INFB	O9qav3 influenza b
881	35	46.7	347	2	O9PC8_9INFB	O9pc8 influenza b	954	35	46.7	347	2	O9QAV4_9INFB	O9qav4 influenza b
882	35	46.7	347	2	O9PC9_9INFB	O9pc9 influenza b	955	35	46.7	347	2	O8ORD2_9INFB	O8ord2 influenza b
883	35	46.7	347	2	O9PC0_9INFB	O9pc0 influenza b	956	35	46.7	347	2	O8JP23_9INFB	O8jp23 influenza b
884	35	46.7	347	2	O9PC1_9INFB	O9pc1 influenza b	957	35	46.7	347	2	O8JP36_9INFB	O8jp36 influenza b
885	35	46.7	347	2	O9PC2_9INFB	O9pc2 influenza b	958	35	46.7	347	2	O91F66_9INFB	O91f66 influenza b
886	35	46.7	347	2	O9PC3_9INFB	O9pc3 influenza b	959	35	46.7	347	2	O9QAV2_9INFB	O9qav2 influenza b
887	35	46.7	347	2	O9PC4_9INFB	O9pc4 influenza b	960	35	46.7	347	2	O8B923_9INFB	O8b923 influenza b
888	35	46.7	347	2	O9PC5_9INFB	O9pc5 influenza b	961	35	46.7	347	2	O8JP24_9INFB	O8jp24 influenza b
889	35	46.7	347	2	O9PC6_9INFB	O9pc6 influenza b	962	35	46.7	347	2	O8JP26_9INFB	O8jp26 influenza b
890	35	46.7	347	2	O9PC7_9INFB	O9pc7 influenza b	963	35	46.7	347	2	O8JP27_9INFB	O8jp27 influenza b
891	35	46.7	347	2	O9PC8_9INFB	O9pc8 influenza b	964	35	46.7	347	2	O8JP34_9INFB	O8jp34 influenza b
892	35	46.7	347	2	O9PC9_9INFB	O9pc9 influenza b	965	35	46.7	347	2	O8JP37_9INFB	O8jp37 influenza b
893	35	46.7	347	2	O9PC0_9INFB	O9pc0 influenza b	966	35	46.7	347	2	O8JP43_9INFB	O8jp43 influenza b
894	35	46.7	347	2	O9PC1_9INFB	O9pc1 influenza b	967	35	46.7	347	2	O8JP52_9INFB	O8jp52 influenza b
895	35	46.7	347	2	O9PC2_9INFB	O9pc2 influenza b	968	35	46.7	347	2	O8JP53_9INFB	O8jp53 influenza b
896	35	46.7	347	2	O9PC3_9INFB	O9pc3 influenza b	969	35	46.7	347	2	O9WSR3_9INFB	O9wsr3 influenza b
897	35	46.7	347	2	O9PC4_9INFB	O9pc4 influenza b	970	35	46.7	347	2	O4CS3_9INFB	O4cs3 influenza b
898	35	46.7	347	2	O9PC5_9INFB	O9pc5 influenza b	971	35	46.7	347	2	O4CO8_9INFB	O4co8 influenza b
899	35	46.7	347	2	O9PC6_9INFB	O9pc6 influenza b	972	35	46.7	347	2	O8ORD1_9INFB	O8ord1 influenza b
900	35	46.7	347	2	O9PC7_9INFB	O9pc7 influenza b	973	35	46.7	347	2	O8ORD3_9INFB	O8ord3 influenza b
901	35	46.7	347	2	O9PC8_9INFB	O9pc8 influenza b	974	35	46.7	347	2	O8JP32_9INFB	O8jp32 influenza b
902	35	46.7	347	2	O9PC9_9INFB	O9pc9 influenza b	975	35	46.7	347	2	O8JP38_9INFB	O8jp38 influenza b
903	35	46.7	347	2	O9PC0_9INFB	O9pc0 influenza b	976	35	46.7	347	2	O8JP42_9INFB	O8jp42 influenza b
904	35	46.7	347	2	O9PC1_9INFB	O9pc1 influenza b	977	35	46.7	347	2	O91F61_9INFB	O91f61 influenza b
905	35	46.7	347	2	O9PC2_9INFB	O9pc2 influenza b	978	35	46.7	347	2	O9WS1_9INFB	O9ws1 influenza b
906	35	46.7	347	2	O9PC3_9INFB	O9pc3 influenza b	979	35	46.7	347	2	O8B9Y6_9INFB	O8b9y6 influenza b
907	35	46.7	347	2	O9PC4_9INFB	O9pc4 influenza b	980	35	46.7	347	2	O8B9Y7_9INFB	O8b9y7 influenza b

981	35	46.7	352	2	Q8B9Y8_91NFB	Q8B9Y8 influenza b
982	35	46.7	352	2	Q8B9Y9_91NFB	Q8B9Y9 influenza b
983	35	46.7	352	2	Q8B9Z2_91NFB	Q8B9Z2 influenza b
984	35	46.7	352	2	Q8B9P8_91NFB	Q8B9P8 influenza b
985	35	46.7	352	2	Q8B9P1_91NFB	Q8B9P1 influenza b
986	35	46.7	352	2	Q8B9P2_91NFB	Q8B9P2 influenza b
987	35	46.7	352	2	Q8B9P3_91NFB	Q8B9P3 influenza b
988	35	46.7	352	2	Q8B9P4_91NFB	Q8B9P4 influenza b
989	35	46.7	352	2	Q8B9P5_91NFB	Q8B9P5 influenza b
990	35	46.7	352	2	Q8B9P6_91NFB	Q8B9P6 influenza b
991	35	46.7	352	2	Q8B9P7_91NFB	Q8B9P7 influenza b
992	35	46.7	352	2	Q8B9P8_91NFB	Q8B9P8 influenza b
993	35	46.7	352	2	Q8B9P9_91NFB	Q8B9P9 influenza b
994	35	46.7	352	2	Q8B9P10_91NFB	Q8B9P10 influenza b
995	35	46.7	352	2	Q8B9P11_91NFB	Q8B9P11 influenza b
996	35	46.7	353	1	HEMA_INBAA	P12440 influenza b
997	35	46.7	353	2	Q8B9P30_91NFB	Q8B9P30 influenza b
998	35	46.7	353	2	Q8B9P47_91NFB	Q8B9P47 influenza b
999	35	46.7	353	2	Q8B9P54_91NFB	Q8B9P54 influenza b
1000	35	46.7	353	2	Q8B9P60_91NFB	Q8B9P60 influenza b

ALIGNMENTS

RESULT 1
FAS_HUMAN STANDARD; PRT; 2351 AA.

AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Coagulation factor VIII precursor (Procoagulant component)
DE (Antithrombotic factor) (AHF) [Contains: Factor VIIa heavy chain, 200
kDa isoform; Factor VIIa heavy chain, 92 kDa isoform; Factor VIII B
chain; Factor VIIa light chain].
GN Name=F8; Synonyms=F8C;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE [MRNA].
RP MEDLINE=86081164; PubMed=3395400;
RA Thruett M.A., Blacher R., Burke R.L., Caput D., Chu C., Dana D.,
RA Harzog K., Kuo C.H., Masiarz F.R., Merryweather J.P., Najarian R.,
RA Pachl C., Potter S.J., Puma J., Quiroga M., Rall L.B., Randolph A.,
RA Urdea M.S., Valenzuela P., Dahl H.-H.M., Favalaro J., Hansen J.,
RA Nordfang O., Ezban M.;
RT "Characterization of the polypeptide composition of human factor
VIII:C and the nucleotide sequence and expression of the human kidney
cDNA.";
RL DNA 4:333-349(1985).
RN NUCLEOTIDE SEQUENCE [MRNA].
RP MEDLINE=85061548; PubMed=6438526;
RA Wood W.I., Capon D.J., Simonsen C.C., Eaton D.L., Gitschier J.,
RA Key B., Seeburg P.H., Smith D.H., Hollingshead P., Wilson K.L.,
RA Delwart E., Tuddenham E.G.D., Vehar G.A., Lawn R.M.;
RT "Expression of active human factor VIII from recombinant DNA clones.";
RL Nature 312:330-337(1984).
RN NUCLEOTIDE SEQUENCE [MRNA].
RP MEDLINE=85061550; PubMed=6438528;
RA Tootle J.W., Knopf J.U., Wozney J.M., Sultzman L.A., Buecker J.L.,
RA Pittman D.D., Kaufman R.J., Brown E., Shoemaker C., Orr E.C.,
RA Amphlett G.W., Foster W.B., Coe M.L., Knutson G.J., Fess D.N.,
RA Hewick R.M.;
RT "Molecular cloning of a cDNA encoding human antithrombotic factor.";
RL Nature 312:342-347(1984).
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RX MEDLINE=93265012; PubMed=1303178;
RA Gitschier J., Wood W.I.;
RT "Sequence of the exon-containing regions of the human factor VIII
gene.";
RL Hum. Mol. Genet. 1:199-200(1992).
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS GLU-1260 AND VAL-2257.
RP Rieder M.J., Daniels R.L., de Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Rajkumar N., Yi Q., Nickerson D.A.;
RT "Sequences, NHLBI H166682 program for genomic applications, UW-
FHRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 2064-2070.
RP de Water N.S., Williams R., Browett P.J.;
RA "Factor VIII gene normal intron 20 sequence.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN SULFATION OF TYR-1699.
RP MEDLINE=91093266; PubMed=1898735;
RA Leyte A., van Schijndel H.B., Niehrs C., Huttner W.B., Verbeet M.P.,
RA Mertens K., van Mourik J.A.;
RT "Sulfation of Tyr1680 of human blood coagulation factor VIII is
essential for the interaction of factor VIII with von Willebrand
factor.";
RL J. Biol. Chem. 266:740-746(1991).
RN SULFATION.
RP MEDLINE=92207952; PubMed=1554716;
RA Pittman D.D., Wang J.H., Kaufman R.J.;
RT "Identification and functional importance of tyrosine sulfate residues
within recombinant factor VIII.";
RL Biochemistry 31:3315-3325(1992).
RN SULFATION SITES TYR-737, TYR-738 AND TYR 742, AND DISULFIDE BONDS.
RP MEDLINE=96338127; PubMed=7613471;
RA McWilliam B.A., Fujikawa K., Davie E.W., Hedner U., Ezban M.;
RT "Locations of disulfide bonds and free cysteines in the heavy and
light chains of recombinant human factor VIII (antithrombotic factor
A).";
RL Protein Sci. 4:740-746(1995).
RN STRUCTURE BY NMR OF 2322-2343.
RP MEDLINE=95200924; PubMed=7893714;
RA Gilbert G.E., Baleja J.D.;
RT "Membrane-binding peptide from the C2 domain of factor VIII forms an
amphipathic structure as determined by NMR spectroscopy.";
RL Biochemistry 34:3022-3031(1995).
RN REVIEW ON MOLECULAR BASIS OF HEMA.
RP MEDLINE=91221499; PubMed=1902642;
RA Gitschier J.;
RT "The molecular basis of hemophilia A.";
RL Ann. N. Y. Acad. Sci. 614:89-96(1991).
RN REVIEW ON MOLECULAR BASIS OF HEMA.
RP MEDLINE=89088506; PubMed=2491949;
RA White G.C. II, Shoemaker C.B.;
RT "Factor VIII gene and hemophilia A.";
RL Blood 73:1-12(1989).
RN REVIEW ON MOLECULAR BASIS OF HEMA.
RP MEDLINE=95245332; PubMed=7728145;
RA Antonarakis S.E., Kazazian H.H. Jr., Tuddenham E.G.D.;
RT "Molecular etiology of factor VIII deficiency in hemophilia A.";
RL Hum. Mutat. 5:11-22(1995).
RN VARIANT HEMA GLN-2326.
RP MEDLINE=86235434; PubMed=3012775;
RA Gitschier J., Wood W.I., Shuman M.A., Lawn R.M.;
RT "Identification of a missense mutation in the factor VIII gene of a
mild hemophilia.";
RL Science 232:1415-1416(1986).

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OM protein - protein search, using SW model

Run on: November 25, 2005, 23:01:59 ; Search time 6.2069 Seconds
(without alignments)
232.524 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect score: 75
Sequence: 1 MSSSPHYLRNNAQSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	2351	1 EZHU	coagulation factor
2	56	74.7	869	2 A25945	coagulation factor
3	56	74.7	2133	2 T42763	coagulation factor
4	50	66.7	440	2 G82426	probable phosphogl
5	43	57.3	2319	2 A47004	coagulation factor
6	42	56.0	355	1 S22181	gamma-1-microglobu
7	40	53.3	133	2 UC7103	endo-1,4-beta-xyla
8	40	53.3	390	2 F83220	hypothetical prote
9	40	53.3	584	2 H95336	probable adenylate
10	40	53.3	616	2 B33586	C4-dicarboxylate t
11	40	53.3	621	2 D96032	hypothetical prote
12	39	52.0	88	2 C64469	hypothetical prote
13	39	52.0	312	2 B86494	integrase/recombin
14	39	52.0	312	2 F72129	integrase/recombin
15	39	52.0	443	2 I38603	heme A faarneyltra
16	38	50.7	101	2 D70710	hypothetical prote
17	38	50.7	174	2 S74666	DnaJ protein - Syn
18	38	50.7	186	2 S46093	probable membrane
19	38	50.7	405	2 UC5175	beed storage prote
20	38	50.7	567	2 E84504	hypothetical prote
21	38	50.7	2414	2 A54277	transcription adap
22	38	50.7	2441	2 S39161	CREB-binding prote
23	37.5	50.0	698	2 G89787	hypothetical prote
24	37	49.3	133	2 A66283	hypothetical prote
25	37	49.3	138	2 AE1089	Antigen C homolog
26	37	49.3	361	2 AG0335	cholesterol synthas
27	37	49.3	383	2 G89902	competence-damage
28	37	49.3	392	2 T51772	acetyl-CoA C-acety
29	37	49.3	650	2 T15972	hypothetical prote

30	37	49.3	1052	2 E71422	hypothetical prote
31	37	49.3	1256	2 T47325	hypothetical prote
32	37	49.3	2275	2 T31323	hypothetical prote
33	36.5	48.7	394	2 E65067	hypothetical prote
34	36.5	48.7	394	2 H85936	probable acyltrans
35	36.5	48.7	394	2 E91091	probable acyltrans
36	36	48.0	62	2 S44153	hypothetical prote
37	36	48.0	153	2 A95281	conserved hypothet
38	36	48.0	227	2 F83097	probable two-compo
39	36	48.0	242	2 G83948	3-oxoacyl-l-acyl ca
40	36	48.0	343	2 T06057	fructose-bisphosph
41	36	48.0	410	2 AC3603	3-methyl-2-oxobuta
42	36	48.0	424	2 T19478	hypothetical prote
43	36	48.0	447	2 D82066	pmbA protein VC253
44	36	48.0	476	2 A71302	conserved hypothet
45	36	48.0	662	2 T44221	probable capid pr
46	36	48.0	662	2 T44036	hypothetical prote
47	36	48.0	925	2 T02811	DNA excision/repai
48	36	48.0	974	2 T29007	translational elonga
49	36	48.0	1173	2 T25539	hypothetical prote
50	36	48.0	1456	2 T01397	LR gag/pol polypyr
51	35.5	47.3	440	2 E82213	benzot histidine k
52	35.5	47.3	790	2 T05576	hypothetical prote
53	35	46.7	137	2 D75337	hypothetical prote
54	35	46.7	175	2 S03756	famH protein precu
55	35	46.7	178	2 H95020	DNA-3-methyladenin
56	35	46.7	187	2 E97892	DNA-3-methyladenin
57	35	46.7	214	2 G84361	hypothetical prote
58	35	46.7	221	2 G72322	glutaredoxin-relat
59	35	46.7	223	2 A36462	probable transmemb
60	35	46.7	227	2 T33094	probable orotate p
61	35	46.7	269	2 T16910	hypothetical prote
62	35	46.7	309	2 AC3257	integrase/recombin
63	35	46.7	329	2 D95409	probable integrase
64	35	46.7	329	2 D95372	probable integrase
65	35	46.7	344	2 PC4185	hemagglutinin 1 ch
66	35	46.7	345	2 JQ1909	hemagglutinin 1 -
67	35	46.7	345	2 JQ1910	hemagglutinin 1 -
68	35	46.7	345	2 JQ1915	hemagglutinin 1 -
69	35	46.7	345	2 JQ1911	hemagglutinin 1 -
70	35	46.7	345	2 JQ1913	hemagglutinin 1 -
71	35	46.7	345	2 JQ1907	hemagglutinin 1 -
72	35	46.7	345	2 JQ1906	hemagglutinin 1 -
73	35	46.7	345	2 JQ1912	hemagglutinin 1 -
74	35	46.7	345	2 JQ1908	hemagglutinin 1 -
75	35	46.7	345	2 JQ1916	hemagglutinin 1 -
76	35	46.7	345	2 S36080	hemagglutinin 1 - in
77	35	46.7	345	2 JQ1914	hemagglutinin 1 -
78	35	46.7	347	2 JQ1902	hemagglutinin 1 -
79	35	46.7	347	2 JQ1901	hemagglutinin 1 -
80	35	46.7	347	2 JQ1904	hemagglutinin 1 -
81	35	46.7	347	2 JQ1905	hemagglutinin 1 -
82	35	46.7	353	1 HMIYBA	hemagglutinin prec
83	35	46.7	359	2 CS5066	tyrosine decarboxy
84	35	46.7	378	2 S11738	hemagglutinin prec
85	35	46.7	394	2 F64992	acetyl-CoA C-acetyl
86	35	46.7	405	2 JQ2147	ORP1 protein - mai
87	35	46.7	420	2 S9131	Kan-1 protein - ra
88	35	46.7	424	2 E87558	cytochrome P450 fa
89	35	46.7	488	2 S78236	ribose-bisphosph
90	35	46.7	496	2 AE0305	probable sugar tra
91	35	46.7	508	2 T07971	aromatic-L-amino-a
92	35	46.7	518	2 A55066	tyrosine decarboxy
93	35	46.7	523	2 T09615	tyrosine decarboxy
94	35	46.7	531	2 B55066	aromatic-L-amino-a
95	35	46.7	533	2 T07970	hypothetical prote
96	35	46.7	563	2 AD2011	hemagglutinin prec
97	35	46.7	574	1 HMIYBM	hemagglutinin prec
98	35	46.7	575	1 HMIYBH	hemagglutinin prec
99	35	46.7	576	2 S01882	hemagglutinin prec
100	35	46.7	576	2 S03300	hemagglutinin prec
101	35	46.7	578	2 S03299	hemagglutinin prec
102	35	46.7	578	2 S03301	hemagglutinin prec

103	35	46.7	583	1	HMTVBS	hemagglutinin prec	176	34	45.3	1115	2	S64101	PAN2 protein - yea
104	35	46.7	583	1	HMTVHO	hemagglutinin prec	177	34	45.3	1182	2	T13952	membrane protein p
105	35	46.7	584	1	HMTVIB	hemagglutinin prec	178	34	45.3	1213	2	A54063	TATA-binding prote
106	35	46.7	585	1	HMTVBJ	hemagglutinin prec	179	34	45.3	1237	2	T46609	calcium-activated
107	35	46.7	607	1	C71367	probable ATP-depen	180	34	45.3	1237	2	A34598	ecdysone-induced p
108	35	46.7	755	2	D75598	photoreceptor - De	181	34	45.3	1298	2	B83175	phosphoribosylform
109	35	46.7	781	2	A13448	xanthine dehydroge	182	34	45.3	1394	2	B34558	ecdysone-induced p
110	35	46.7	1078	2	D87647	hypothetical prote	183	34	45.3	1443	2	S05979	steroid hormone re
111	35	46.7	1102	2	A84480	hypothetical prote	184	34	45.3	1678	2	D86481	189.6K hypothetica
112	35	46.7	1311	2	T33757	probable retroelem	185	34	45.3	2700	2	D88450	protein F21H11.2 [
113	35	46.7	1784	2	A49420	hypothetical prote	186	34	45.3	5762	2	A41819	proline-rich pepti
114	35	46.7	1809	2	S57329	tuberos sclerosi	187	33.5	44.7	389	2	G70759	probable, fadA pro
115	35	46.7	2111	2	T15390	hypothetical prote	188	33.5	44.7	395	2	T51774	acetyl-CoA C-acety
116	35	46.7	2496	2	A71616	secreted protein p	189	33.5	44.7	418	2	T36965	hypothetical prote
117	34.5	46.0	391	2	B83155	probable acyl-CoA	190	33	44.0	105	2	T06513	emc1 protein - ga
118	34.5	46.0	392	2	A80868	acetyl-CoA C-acety	191	33	44.0	131	2	C75526	hypothetical prote
119	34.5	46.0	396	2	G83326	probable acyl-CoA	192	33	44.0	162	2	B86637	acetyl transferase
120	34.5	46.0	607	2	S88151	probable acyl-CoA	193	33	44.0	162	2	AG1077	PTS system, fructo
121	34	45.3	106	2	UC7778	hepatocyte growth	194	33	44.0	162	2	AF1435	PTS system, fructo
122	34	45.3	209	2	C82656	hypothetical prote	195	33	44.0	163	2	S14269	phenomene-binding
123	34	45.3	251	2	G96006	probable SUR1-like	196	33	44.0	169	2	T08823	disease resistance
124	34	45.3	265	2	T40757	conserved hypothet	197	33	44.0	186	2	G75474	probable acetyltra
125	34	45.3	282	2	AF0902	dihydropterate sy	198	33	44.0	186	2	B91133	hypothetical prote
126	34	45.3	286	2	AF2267	hypothetical prote	199	33	44.0	186	2	B85978	hypothetical prote
127	34	45.3	297	2	T34141	hypothetical prote	200	33	44.0	186	2	B5105	hypothetical prote
128	34	45.3	306	2	G82763	pteridine-dependen	201	33	44.0	191	2	T19804	hypothetical prote
129	34	45.3	329	2	AH3121	conserved hypothet	202	33	44.0	191	2	T19803	hypothetical prote
130	34	45.3	329	2	G98165	hypothetical prote	203	33	44.0	202	2	H58930	ribosomal protein
131	34	45.3	347	2	U01903	hemagglutinin 1 -	204	33	44.0	205	2	AG0917	threonine efflux p
132	34	45.3	354	2	D84955	hypothetical prote	205	33	44.0	211	2	G97376	hypothetical prote
133	34	45.3	360	2	AD1929	hypothetical prote	206	33	44.0	220	2	T73358	hypothetical prote
134	34	45.3	361	1	SYEBKR	choistamate synthas	207	33	44.0	227	2	T42160	probable Klr prote
135	34	45.3	361	2	AF0804	choistamate synthas	208	33	44.0	234	2	AF2594	conserved hypothet
136	34	45.3	364	2	AD3440	choistamate synthas	209	33	44.0	237	2	H83719	hypothetical prote
137	34	45.3	365	2	AD2669	choistamate synthas	210	33	44.0	242	2	C82575	phage-related prot
138	34	45.3	368	2	B97451	ornithine synthas	211	33	44.0	267	2	S09672	kafirin precursor
139	34	45.3	375	2	UC8029	ornithine carboxy	212	33	44.0	269	2	S04124	kafirin precursor
140	34	45.3	393	1	XXALAE	acetyl-CoA C-acety	213	33	44.0	275	2	G75606	D-alanine transam
141	34	45.3	400	2	T10476	cell division prot	214	33	44.0	293	3	AB3555	probable integrase
142	34	45.3	416	2	B84030	stage VI sporulati	215	33	44.0	298	1	A64061	site-specific inte
143	34	45.3	425	2	B84919	hypothetical prote	216	33	44.0	297	1	A39202	site-specific inte
144	34	45.3	460	1	UC1417	DNA repair protein	217	33	44.0	298	2	AB0872	site-specific inte
145	34	45.3	460	2	AC1074	probable DNA repai	218	33	44.0	298	2	B85945	site-specific reco
146	34	45.3	460	2	E86138	probable ATP-depen	219	33	44.0	298	2	F91099	site-specific reco
147	34	45.3	460	2	C91297	probable ATP-depen	220	33	44.0	299	2	AE0109	integrase/recombin
148	34	45.3	465	2	H95369	Eg1c KMDO-1,3-1,4-	221	33	44.0	301	2	B65933	GRP-binding protei
149	34	45.3	466	1	WMBERT	capsid protein ICP	222	33	44.0	302	1	D69035	Mu132 protein hom
150	34	45.3	469	2	B84644	probable protein K	223	33	44.0	302	2	A82080	integrase/recombin
151	34	45.3	496	2	T48812	hypothetical prote	224	33	44.0	305	2	T47844	hypothetical prote
152	34	45.3	500	1	ITRHUC1	complement C1 inh	225	33	44.0	305	2	T05053	probable MYB fam1
153	34	45.3	521	2	T27192	hypothetical prote	226	33	44.0	309	2	S72959	integrase
154	34	45.3	524	2	S46007	hypothetical prote	227	33	44.0	316	1	G87079	integrase/recombin
155	34	45.3	523	2	T49061	hypothetical prote	228	33	44.0	316	2	C70438	conserved hypothet
156	34	45.3	569	2	S11035	chaperonin hsp60,	229	33	44.0	316	2	H82681	integrase/recombin
157	34	45.3	583	2	S56680	beta-fructofuranos	230	33	44.0	324	2	T05303	hypothetical prote
158	34	45.3	597	2	T10034	hypothetical prote	231	33	44.0	326	2	T01944	hypothetical prote
159	34	45.3	597	2	D86915	conserved hypothet	232	33	44.0	328	2	T26714	hypothetical prote
160	34	45.3	608	2	C72405	hydrogenase (BC 1.	233	33	44.0	331	2	AC3003	site-specific reco
161	34	45.3	618	2	TC4366	transcription fact	234	33	44.0	331	2	P98280	integrase/recombin
162	34	45.3	620	2	T15773	hypothetical prote	235	33	44.0	337	2	B30076	hypothetical prote
163	34	45.3	675	2	S53831	NADH2 dehydrogenas	236	33	44.0	337	2	PC4365	calcium-binding pr
164	34	45.3	678	2	E86909	probable DNA gyras	237	33	44.0	342	2	T28772	hypothetical prote
165	34	45.3	697	2	T10005	DNA topoisomerase	238	33	44.0	348	2	T51376	plant adhesion mol
166	34	45.3	723	2	H82035	fatty oxidation co	239	33	44.0	356	2	T23802	hypothetical prote
167	34	45.3	736	2	T03849	Fas-binding protei	240	33	44.0	358	2	SYECKR	choistamate synthas
168	34	45.3	740	2	T03847	Fas-binding protei	241	33	44.0	361	1	B91030	choistamate synthas
169	34	45.3	752	2	T44142	DRI protein [impor	242	33	44.0	361	2	F85874	choistamate synthas
170	34	45.3	779	2	T13078	KIAA0992 protein -	243	33	44.0	361	2	B81055	choistamate synthas
171	34	45.3	1008	2	T18727	hypothetical prote	244	33	44.0	366	2	AB1822	choistamate synthas
172	34	45.3	1012	2	T18724	hypothetical prote	245	33	44.0	377	1	VH1H79	nucleocapsid prote
173	34	45.3	1016	2	T25433	hypothetical prote	246	33	44.0	392	2	B83899	thiolase (acetyl-C
174	34	45.3	1025	2	B86145	hypothetical prote	247	33	44.0				
175	34	45.3	1045	1	SYEXI	isoletucine-tRNA 11	248	33	44.0	401	2	A85758	probable oxidoredu

249	33	44.0	401	2	B64877	probable membrane
250	33	44.0	401	2	D90861	probable
251	33	44.0	406	2	S5549	serotonin 4 recept
252	33	44.0	406	2	G72244	hypothetical prote
253	33	44.0	407	2	S53900	hypothetical prote
254	33	44.0	429	2	B83257	folypolyglutamate
255	33	44.0	429	2	G75114	hypothetical prote
256	33	44.0	434	2	A10317	hypothetical prote
257	33	44.0	437	2	CG4113	tetrahydrofolypol
258	33	44.0	448	2	T51188	hypothetical prote
259	33	44.0	453	2	B69504	beetyl-cRNA synthe
260	33	44.0	466	2	A82605	conjugal transfer
261	33	44.0	469	2	AD1926	hypothetical prote
262	33	44.0	477	2	S52162	sucrose hydrolase
263	33	44.0	477	2	C91034	sucrose-6 phosphat
264	33	44.0	477	2	D85878	sucrose hydrolase
265	33	44.0	482	2	G02058	retinoic acid- and
266	33	44.0	482	2	T16695	hypothetical prote
267	33	44.0	502	2	S36494	E2 protein - human
268	33	44.0	503	2	C84595	similar to PEARL
269	33	44.0	514	2	T49965	hypothetical prote
270	33	44.0	519	2	C71346	probable transcrip
271	33	44.0	558	2	S68447	origin recognition
272	33	44.0	583	2	A70723	probable acyl-coas
273	33	44.0	621	2	T15859	hypothetical prote
274	33	44.0	656	2	T37941	conserved hypotet
275	33	44.0	657	2	T52460	hypothetical prote
276	33	44.0	673	2	T47905	hypothetical prote
277	33	44.0	690	2	S28222	peroxidase (EC 1.1
278	33	44.0	690	2	S35251	probable membrane
279	33	44.0	694	2	G95314	probable site-spec
280	33	44.0	736	2	D86271	protein Pl6A14.2 [
281	33	44.0	740	2	T24340	hypothetical prote
282	33	44.0	775	1	VEXRHK	outer layer protei
283	33	44.0	775	1	VEXRW4	outer layer protei
284	33	44.0	775	1	VEXRMS	outer layer protei
285	33	44.0	775	1	VEXRWP	outer layer protei
286	33	44.0	775	1	VEXRML	outer layer protei
287	33	44.0	775	1	VEXRWM	outer layer protei
288	33	44.0	775	1	S52165	outer capsid prote
289	33	44.0	797	2	T33927	hypothetical prote
290	33	44.0	798	2	S29815	N-ras upstream pro
291	33	44.0	798	2	S11210	probable unr prote
292	33	44.0	841	2	T48508	beta-adaptin-like
293	33	44.0	866	2	T06454	probable lipoxgen
294	33	44.0	889	2	T09055	protocaderin 68 -
295	33	44.0	1027	2	H87316	hypothetical prote
296	33	44.0	1036	2	S76027	hypothetical prote
297	33	44.0	1048	2	S57155	NMD5 protein - Yea
298	33	44.0	1082	2	S64903	regulatory protein
299	33	44.0	1153	2	S00551	leukocyte surface
300	33	44.0	1163	2	G97236	AtApase involved in
301	33	44.0	1216	2	H85023	hypothetical prote
302	33	44.0	1268	2	T31420	C-terminal domain-
303	33	44.0	1326	2	S65395	secretory phosphol
304	33	44.0	1363	2	T15653	hypothetical prote
305	33	44.0	1463	2	A53210	phospholipase A2 r
306	33	44.0	1465	2	A56395	secretory phosphol
307	33	44.0	1791	2	T02345	hypothetical prote
308	33	44.0	2030	2	T31162	hypothetical prote
309	33	44.0	2180	2	A46182	polypotein - echo
310	33	44.0	2214	1	OZBYU2	pyrimidine synthe
311	33	44.0	234	2	A82960	transcription regu
312	33	44.0	234	2	D98323	transcription regu
313	33	44.0	258	2	T30368	probable immediate
314	33	44.0	377	2	F71520	hypothetical prote
315	33	44.0	405	2	B82752	hypothetical prote
316	33	44.0	417	2	B98299	cystathionine gamm
317	33	44.0	417	2	A82984	probable acyl-CoA
318	33	44.0	417	2	A82984	acetyl-CoA C-acety
319	33	44.0	100	2	T06836	ribosomal protein
320	33	44.0	115	1	G64304	30S ribosomal prot
321	33	44.0	120	2	A72676	hypothetical prote
						probable GAGE-2 pr
322	32	42.7	165	2	T06998	probable H+-transp
323	32	42.7	211	2	S87632	conserved hypotet
324	32	42.7	225	2	S67772	hypothetical prote
325	32	42.7	231	2	AE2164	hypothetical prote
326	32	42.7	245	2	F95420	conserved hypotet
327	32	42.7	253	2	T06113	conserved hypotet
328	32	42.7	259	2	A55274	hypothetical prote
329	32	42.7	259	2	S65744	3-oxo-5alpha-stero
330	32	42.7	276	2	G87296	steroid 5alpha-red
331	32	42.7	279	2	C82915	hydroxylase, alpha/b
332	32	42.7	285	2	H85356	ribosomal protein
333	32	42.7	289	2	S70547	hypothetical prote
334	32	42.7	303	2	G86668	SaBP protein - Sai
335	32	42.7	304	2	G83820	GTP-binding protei
336	32	42.7	306	2	C97761	integrase/recombin
337	32	42.7	306	2	AE1394	conserved hypotet
338	32	42.7	311	2	D70503	probable integrase
339	32	42.7	311	2	AH2153	hypothetical prote
340	32	42.7	318	2	AC2442	hypothetical prote
341	32	42.7	322	2	H85474	hypothetical prote
342	32	42.7	334	2	A29561	prostatic spermine
343	32	42.7	335	2	B71693	integrase/recombin
344	32	42.7	341	2	JB0325	Int protein - huma
345	32	42.7	345	2	G83728	phosphoribosylamin
346	32	42.7	346	2	H69873	conserved hypotet
347	32	42.7	351	2	T09887	DNA-binding protei
348	32	42.7	362	2	B87571	hypothetical prote
349	32	42.7	362	2	F97451	chaperone protein
350	32	42.7	364	1	DEBYO	dihydroorotase (EC
351	32	42.7	371	2	AH2669	molecular chaperon
352	32	42.7	378	2	AC2597	conserved hypotet
353	32	42.7	378	2	C97379	hypothetical prote
354	32	42.7	379	2	D82801	molybdopterin bios
355	32	42.7	379	2	E95946	probable enzyme pr
356	32	42.7	392	2	E84783	probable giberelli
357	32	42.7	395	2	D85960	cystathionine beta
358	32	42.7	395	2	D91115	phosphoprotein - N
359	32	42.7	395	2	S22827	acetyl-CoA C-acety
360	32	42.7	397	1	XURT	hypothetical prote
361	32	42.7	402	2	S31196	globulin 2 - eaate
362	32	42.7	410	2	S18157	hypothetical prote
363	32	42.7	417	2	T47616	gene 68 protein -
364	32	42.7	418	1	WZBER9	2-oxoisovalerate d
365	32	42.7	419	2	T04530	hypothetical prote
366	32	42.7	419	2	D85334	hypothetical prote
367	32	42.7	424	2	T42662	hypothetical prote
368	32	42.7	428	2	AH2963	2-oxoisovalerate d
369	32	42.7	428	2	G98084	gene IV protein -
370	32	42.7	428	2	S08084	hypothetical prote
371	32	42.7	441	2	T32021	acetyl-CoA C-acety
372	32	42.7	445	2	A64092	hypothetical prote
373	32	42.7	448	2	C83793	hypothetical prote
374	32	42.7	449	2	F75558	hypothetical prote
375	32	42.7	451	1	C64186	pmbA protein - Hae
376	32	42.7	451	2	G87437	hypothetical prote
377	32	42.7	451	2	S58334	glutamate-5-semial
378	32	42.7	462	2	AD1284	menaquinone-spezif
379	32	42.7	462	2	AG1655	menaquinone-spezif
380	32	42.7	462	2	A70518	probable lipJ prot
381	32	42.7	463	2	JS0376	hypothetical 53.0K
382	32	42.7	465	2	D88448	protein C45G9.8 [i
383	32	42.7	468	2	T26081	hypothetical prote
384	32	42.7	468	2	H82865	conjugal transfer
385	32	42.7	473	2	F89931	dhNADPoisamide d
386	32	42.7	479	2	A84588	probable tyrosine
387	32	42.7	485	2	C69814	benzaldehyde dehyd
388	32	42.7	488	2	S18156	globulin 1 - eaate
389	32	42.7	502	2	T26256	hypothetical prote
390	32	42.7	511	2	UC7682	spermatogenesis as
391	32	42.7	514	2	D81952	type I site-specific
392	32	42.7	514	2	F81152	type I restriction
393	32	42.7	515	2	S54592	hypothetical prote
394	32	42.7	517	1	S19243	tyrosinase-related

395	32	42.7	517	2	T03445	glucose-1-phosphat	
396	32	42.7	519	1	YRHUR2	dopachrome isomera	
397	32	42.7	520	3	C81424	cytochrome bd oxid	
398	32	42.7	523	4	D55066	probable tyrosine	
399	32	42.7	535	2	C84699	probable CDC6 prot	
400	32	42.7	545	2	D69679	polyketide synthas	
401	32	42.7	553	2	T27245	hypothetical prote	
402	32	42.7	565	1	VH1VC8	nucleoprotein - in	
403	32	42.7	566	2	H84203	phosphatase ABC tran	
404	32	42.7	568	2	H88904	protein Y57G11C.9	
405	32	42.7	569	2	T22516	hypothetical prote	
406	32	42.7	580	2	T46024	hypothetical prote	
407	32	42.7	586	2	JC6500	hmf-3/forhead tra	
408	32	42.7	592	2	E89772	hypothetical prote	
409	32	42.7	593	2	A10850	pathogenicity isla	
410	32	42.7	593	2	E70216	slb protein - Sal	
411	32	42.7	617	2	E72803	gp1 protein - Myc	
412	32	42.7	633	2	AC0581	penicillin-binding	
413	32	42.7	643	2	T19549	hypothetical prote	
414	32	42.7	644	2	B31794	mdm-1 protein (c1o	
415	32	42.7	647	2	T43952	hypothetical prote	
416	32	42.7	659	2	T27246	hypothetical prote	
417	32	42.7	663	2	T40493	hmf-3/forhead tra	
418	32	42.7	685	2	C70678	probable electon	
419	32	42.7	692	2	T06593	arginine decarboxy	
420	32	42.7	692	2	T15819	hypothetical prote	
421	32	42.7	700	2	C86296	hypothetical prote	
422	32	42.7	762	2	H83415	cis/trans isomeras	
423	32	42.7	764	2	S48521	AK1 protein - yea	
424	32	42.7	783	2	T23452	hypothetical prote	
425	32	42.7	785	2	T23456	hypothetical prote	
426	32	42.7	798	2	T48304	hypothetical prote	
427	32	42.7	804	2	T14762	hypothetical prote	
428	32	42.7	808	2	J02205	Uil47h protein - Ma	
429	32	42.7	831	2	JC7880	glucosylceramidase	
430	32	42.7	870	2	A89201	protein F32D8.4 (l	
431	32	42.7	878	2	T21621	hypothetical prote	
432	32	42.7	912	2	T21659	hypothetical prote	
433	32	42.7	1011	2	S11177	vacuolar sorting p	
434	32	42.7	1015	2	B87992	protein W09G3.1a (
435	32	42.7	1025	2	S50293	probable membrane	
436	32	42.7	1040	2	E71412	hypothetical prote	
437	32	42.7	1053	2	T51016	related to Cyc8 pr	
438	32	42.7	1081	2	S51899	probable protein k	
439	32	42.7	1103	2	H82884	multiple banded an	
440	32	42.7	1151	2	T38424	hypothetical prote	
441	32	42.7	1153	1	RMHUIB	cell surface glyco	
442	32	42.7	1170	2	S30010	probable finger pr	
443	32	42.7	1197	2	T13956	limbless protein h	
444	32	42.7	1230	2	T18256	probable serine/ch	
445	32	42.7	1230	2	T18259	serine/threonine p	
446	32	42.7	1233	1	G71612	novel serine/threo	
447	32	42.7	1293	2	T30871	orexin-like acid by	
448	32	42.7	1309	2	T13158	adenylate cyclase	
449	32	42.7	1330	2	S49010	embryonic receptor	
450	32	42.7	1333	2	T78875	receptor tyrosine	
451	32	42.7	1374	2	B85188	reticulandposon 1i	
452	32	42.7	1535	2	S46224	peroxidasin - frui	
453	32	42.7	1545	2	T26589	hypothetical prote	
454	32	42.7	1626	2	T26318	hypothetical prote	
455	32	42.7	1748	1	JN0786	integrin beta-4 ch	
456	32	42.7	1872	2	JC4976	plexin 3 precursor	
457	32	42.7	2088	2	E71436	hypothetical prote	
458	32	42.7	2124	2	T01526	hypothetical prote	
459	32	42.7	2352	2	T06077	splicing factor PR	
460	32	42.7	2359	2	B96832	hypothetical prote	
461	32	42.7	3119	2	I49729	HD protein - mouse	
462	32	42.7	3412	1	GNWV7B	genome polyprotein	
463	32	42.7	3414	1	GNWVNE	genome polyprotein	
464	31.5	42.0	3414	1	HSUR1B	histone H1, gonada	
465	31.5	42.0	355	1	TS1442	seed maturation-1i	
466	31.5	42.0	368	2	AB2846	Ca2+/H+ antiporter	
467	31.5	42.0	368	2	B97623	cpaA protein (A000	
468	469	31.5	42.0	947	2	B86231	hypothetical prote
469	470	31	41.3	93	2	B83358	hypothetical prote
470	471	31	41.3	101	2	E86544	hypothetical prote
471	472	31	41.3	101	2	B72079	hypothetical prote
472	473	31	41.3	115	2	AD0872	conserved hypothet
473	474	31	41.3	118	2	G84322	50S ribosomal prot
474	475	31	41.3	121	2	F72605	hypothetical prote
475	476	31	41.3	130	2	E72651	hypothetical prote
476	477	31	41.3	132	2	AE0224	flagellar protein
477	478	31	41.3	135	2	AB0751	hypothetical prote
478	479	31	41.3	141	2	P95368	hypothetical prote
479	480	31	41.3	149	2	F72597	hypothetical prote
480	481	31	41.3	149	2	B71067	hypothetical prote
481	482	31	41.3	151	2	AG2279	hypothetical prote
482	483	31	41.3	154	2	FE4026	hypothetical prote
483	484	31	41.3	159	1	MMVZU1	T3A protein - shae
484	485	31	41.3	161	2	B29504	hypothetical 18k p
485	486	31	41.3	167	2	T58352	pleiNK4a - mouse
486	487	31	41.3	175	2	S48546	hypothetical prote
487	488	31	41.3	176	2	T47743	hypothetical prote
488	489	31	41.3	177	2	A47207	phycocerythrin beta
489	490	31	41.3	183	2	G83642	DNA-3-methyladenin
490	491	31	41.3	186	2	T37815	hypothetical prote
491	492	31	41.3	197	2	S35252	proline-rich prote
492	493	31	41.3	199	2	E75637	probable chromosom
493	494	31	41.3	207	2	T20391	hypothetical prote
494	495	31	41.3	211	2	AB3178	glutathione S-tran
495	496	31	41.3	212	2	T29480	hypothetical prote
496	497	31	41.3	222	2	F82353	conserved hypothet
497	498	31	41.3	224	2	C83777	hypothetical prote
498	499	31	41.3	226	2	T30695	probable uracil DN
499	500	31	41.3	238	2	C37416	bloodstream-specific
500	501	31	41.3	239	2	B90234	conserved hypothet
501	502	31	41.3	242	2	C95888	hypothetical prote
502	503	31	41.3	247	1	JC6540	placenta specific-
503	504	31	41.3	250	2	T19286	hypothetical prote
504	505	31	41.3	261	2	E69455	conserved hypothet
505	506	31	41.3	262	2	S45026	ribosomal protein
506	507	31	41.3	267	2	H75429	transcription regu
507	508	31	41.3	273	2	B83116	50S ribosomal prot
508	509	31	41.3	273	2	B83119	hypothetical prote
509	510	31	41.3	275	2	T48696	mRNA splicing fact
510	511	31	41.3	277	2	A37416	bloodstream-specific
511	512	31	41.3	282	1	A43326	dihydropteroate by
512	513	31	41.3	282	1	H43255	hydrogenase-1 cofa
513	514	31	41.3	282	2	G71334	probable lysophosp
514	515	31	41.3	287	2	B95858	probable dehydroge
515	516	31	41.3	288	2	G72634	hypothetical prote
516	517	31	41.3	291	2	T01241	probable MYB fam1
517	518	31	41.3	293	2	G75274	nitrilase-related
518	519	31	41.3	293	2	A82967	probable transcrip
519	520	31	41.3	296	2	A10443	probable 2-hydroxy
520	521	31	41.3	296	2	I40818	phosphotransbutyry
521	522	31	41.3	296	2	A64110	cell division inh
522	523	31	41.3	296	2	G97059	ERA GTPase [import
523	524	31	41.3	297	2	H91135	7,8-dihydropteroat
524	525	31	41.3	297	2	C85981	7,8-dihydropteroat
525	526	31	41.3	298	2	F83177	integrinase/recombin
526	527	31	41.3	300	2	A32837	transcription acti
527	528	31	41.3	301	2	E97278	phosphate butyryl
528	529	31	41.3	302	2	C71332	probable smf prote
529	530	31	41.3	305	2	T49208	hypothetical prote
530	531	31	41.3	305	2	A38422	inulin-like prote
531	532	31	41.3	312	2	F71922	acetyl-Coenzyme A
532	533	31	41.3	312	2	E64589	acetyl-CoA cozyme
533	534	31	41.3	312	2	E70185	mevalonate pyropho
534	535	31	41.3	314	2	AC0603	aspartaginase (BC 3
535	536	31	41.3	314	2	AC2878	aromatic compounds
536	537	31	41.3	314	2	A86432	protein T518.11 (I
537	538	31	41.3	315	2	AF3270	integrinase [impor
538	539	31	41.3	323	2	T47447	sulfotransferase-1
539	540	31	41.3	325	2	E97654	ABC transporter no
540	540	31	41.3	333	2	T26162	hypothetical prote

541	31	41.3	334	2	A85067	hypothetical prote	614	31	41.3	551	2	T22121	hypothetical prote
542	31	41.3	336	2	JC4102	hypothetical 36.9k	615	31	41.3	573	2	T49610	related to rna bin
543	31	41.3	337	2	E95423	RebB2 replication	616	31	41.3	582	2	C71424	hypothetical prote
544	31	41.3	339	2	T33477	hypothetical prote	617	31	41.3	583	2	T04327	phosphoglucumutase
545	31	41.3	340	2	A52433	VSG expression sit	618	31	41.3	583	2	T04326	phosphoglucumutase
546	31	41.3	347	2	AD1920	ABC phosphate tran	619	31	41.3	583	2	T12574	phosphoglucumutase
547	31	41.3	347	2	B81243	twitching motility	620	31	41.3	595	2	H95899	hypothetical prote
548	31	41.3	347	2	C82016	probable pilus ret	621	31	41.3	596	2	I38228	Shb protein - huma
549	31	41.3	350	2	AF2294	uroporphyrinogen d	622	31	41.3	601	2	AE3506	sensor protein chv
550	31	41.3	364	2	G82734	acetylornithine de	623	31	41.3	612	2	S65213	hypothetical prote
551	31	41.3	369	2	T04947	hypothetical prote	624	31	41.3	613	2	S27770	hypothetical prote
552	31	41.3	374	2	A31382	DNA-binding protei	625	31	41.3	620	2	A81903	probable chaperone
553	31	41.3	378	2	H69280	NADH-dependent fla	626	31	41.3	620	2	B81118	chaperone protein
554	31	41.3	379	2	G75357	diaminopimelate de	627	31	41.3	620	2	F84638	hypothetical prote
555	31	41.3	381	2	F69666	iron-sulfur cofact	628	31	41.3	621	2	T15046	arginine decarboxy
556	31	41.3	381	2	UC4639	silent information	629	31	41.3	624	2	S44938	nitrogen permease
557	31	41.3	383	2	D71424	hypothetical prote	630	31	41.3	633	1	ZPECP2	penicillin-binding
558	31	41.3	389	2	AD1918	alcohol dehydrogen	631	31	41.3	633	2	A90713	penicillin-binding
559	31	41.3	393	2	F75442	acetyl-CoA acetyl	632	31	41.3	633	2	B85563	penicillin-binding
560	31	41.3	395	2	D97155	stage IV sporulati	633	31	41.3	633	2	C84475	hypothetical prote
561	31	41.3	399	2	B86756	hypothetical prote	634	31	41.3	642	1	S34416	transcription fact
562	31	41.3	401	2	B37416	bloodstream-specif	635	31	41.3	652	2	T20046	hypothetical prote
563	31	41.3	401	2	B32433	VSG expression sit	636	31	41.3	656	2	S55262	UV-endonuclease -
564	31	41.3	402	2	F83422	conserved hypotet	637	31	41.3	657	2	T41546	hypothetical prote
565	31	41.3	410	2	S77661	hypothetical prote	638	31	41.3	666	2	I52648	class A helix-loop
566	31	41.3	416	2	S22611	transcription initia	639	31	41.3	666	2	T05432	hypothetical prote
567	31	41.3	418	2	T45807	transcription fact	640	31	41.3	667	2	A41311	transcription fact
568	31	41.3	421	2	C82253	folylpolyglutamate	641	31	41.3	667	2	F69155	hypothetical prote
569	31	41.3	422	2	T06388	alpha-galactosidas	642	31	41.3	668	2	A46013	coagulation factor
570	31	41.3	423	2	T16750	hypothetical prote	643	31	41.3	670	2	C86432	protein T518.13 [i
571	31	41.3	427	2	I51580	XFGH2 protein - Af	644	31	41.3	681	2	B88158	transcription fact
572	31	41.3	427	2	AC1394	human N-acetylgluc	645	31	41.3	682	2	A42121	basic-helix-loop-h
573	31	41.3	427	2	AP1769	weakly human N-ace	646	31	41.3	682	2	C45020	transcription fact
574	31	41.3	428	2	A53689	transcription fact	647	31	41.3	691	2	S78135	NMDH2 dehydrogenas
575	31	41.3	429	2	A80057	threonine synthase	648	31	41.3	692	2	AD1857	hypothetical prote
576	31	41.3	432	2	T31660	hypothetical prote	649	31	41.3	706	2	S19958	basic helix-loop-h
577	31	41.3	436	2	A70923	hypothetical prote	650	31	41.3	707	2	A46691	E-box-binding prot
578	31	41.3	436	2	T36104	conserved hypotet	651	31	41.3	708	2	T34098	hypothetical prote
579	31	41.3	439	2	AH2093	dihydroorotase [im	652	31	41.3	710	2	S72497	oligopeptide trans
580	31	41.3	440	2	G71522	probable phosphosh	653	31	41.3	711	2	D83897	catalase kate [imp
581	31	41.3	445	2	JC2525	UDP-glucose dehydr	654	31	41.3	714	2	AF2458	hypothetical prote
582	31	41.3	446	2	A55021	beta-cell E-box tr	655	31	41.3	719	2	S61046	AR1 protein - yea
583	31	41.3	446	2	D95061	sensor histidine k	656	31	41.3	733	2	S56277	probable membrane
584	31	41.3	446	2	H97929	histidine kinase (657	31	41.3	734	2	T48565	hypothetical prote
585	31	41.3	446	2	B87912	protein B0205.6 [i	658	31	41.3	735	2	F96701	hypothetical prote
586	31	41.3	454	2	A82587	conserved hypotet	659	31	41.3	755	2	T19558	hypothetical prote
587	31	41.3	454	2	S72481	probable transpos	660	31	41.3	756	2	C84682	hypothetical prote
588	31	41.3	454	2	C82682	glutamate-cysteine	661	31	41.3	760	2	H84427	hypothetical prote
589	31	41.3	458	2	S67054	probable membrane	662	31	41.3	776	2	T51911	related to protein
590	31	41.3	461	2	S60253	ael-12 protein - C	663	31	41.3	779	2	AC2249	heterocyst differe
591	31	41.3	462	2	AH1566	galactosamine-cont	664	31	41.3	782	2	T48722	hypothetical prote
592	31	41.3	468	2	T33516	hypothetical prote	665	31	41.3	784	2	T45697	hypothetical prote
593	31	41.3	470	2	D87485	glutamy1-tRNA synt	666	31	41.3	787	2	A71642	penicillin-binding
594	31	41.3	473	2	H72744	probable D-lactate	667	31	41.3	788	1	JDVLHM	DNA-directed DNA p
595	31	41.3	474	2	B83392	probable transcrip	668	31	41.3	790	2	E97855	penicillin-binding
596	31	41.3	475	1	UBPFG	tubulin gamma chai	669	31	41.3	795	2	T07709	hypothetical prote
597	31	41.3	478	2	T32476	probable protein-c	670	31	41.3	798	2	A40526	integrin beta-7 ch
598	31	41.3	479	2	T15427	hypothetical prote	671	31	41.3	805	2	S73374	phenylalanine-tRNA
599	31	41.3	486	2	S31805	VPS protein - porc	672	31	41.3	818	2	T02436	proline-rich prote
600	31	41.3	486	2	S15470	NS3 protein - hum	673	31	41.3	865	2	T46651	transcription acti
601	31	41.3	490	2	I50708	basic helix-loop-h	674	31	41.3	867	2	T14777	hypothetical prote
602	31	41.3	493	2	S78384	acetyl-CoA carboxy	675	31	41.3	896	2	T51891	hypothetical prote
603	31	41.3	495	2	T31944	hypothetical prote	676	31	41.3	902	2	T41051	hypothetical prote
604	31	41.3	497	2	F83651	hypothetical prote	677	31	41.3	907	2	I50404	beta transducin -
605	31	41.3	500	2	A11913	apolipoprotein N-a	678	31	41.3	913	2	T31497	hypothetical prote
606	31	41.3	513	2	C75553	hypothetical prote	679	31	41.3	915	2	S38090	hypothetical prote
607	31	41.3	515	2	S54453	ecdysteroid UDP-gl	680	31	41.3	932	2	T21338	hypothetical prote
608	31	41.3	517	2	C83642	probable sulfate t	681	31	41.3	942	2	S53963	MGSI protein - yea
609	31	41.3	528	2	S24344	glucose transport	682	31	41.3	954	2	T19765	hypothetical prote
610	31	41.3	532	2	D86966	beta-mannanase Man	683	31	41.3	979	2	JH0589	glutamate receptor
611	31	41.3	538	2	D83946	hypothetical prote	684	31	41.3	979	2	JH0592	glutamate receptor
612	31	41.3	545	2	F83280	probable chemotaxi	685	31	41.3	980	2	I57936	C-term Iyvi1-tRNA
613	31	41.3	546	2	B40407	sterol carrier pro	686	31	41.3	1039	2	C87083	

687	31	41.3	1063	2	T34097	probable protein-t
688	31	41.3	1085	2	S55352	Ifp1 protein - yea
689	31	41.3	1091	1	PL0009	complement C3d/Eps
690	31	41.3	1093	1	S50614	regulatory protein
691	31	41.3	1102	2	T28666	protein kinase C- α
692	31	41.3	1112	2	S49432	replicase 126K - O
693	31	41.3	1118	2	A48292	mucin, tracheobron
694	31	41.3	1120	2	T14275	myosin-like protei
695	31	41.3	1165	2	S62982	vacuolar protein V
696	31	41.3	1181	2	T30578	myosin IC - slime
697	31	41.3	1224	2	F66795	hypothetical prote
698	31	41.3	1237	2	T45070	hypothetical prote
699	31	41.3	1256	2	S14556	asparagine-rich pr
700	31	41.3	1320	2	H64090	phosphoribosylform
701	31	41.3	1366	2	C85077	probable polyprote
702	31	41.3	1384	2	S78132	DNA-directed RNA p
703	31	41.3	1440	2	T27942	lin-15b protein -
704	31	41.3	1459	2	S50437	hypothetical prote
705	31	41.3	1526	2	S49763	gingipain R (EC 3.
706	31	41.3	1538	2	E70874	probable ppsb prot
707	31	41.3	1538	2	AD1512	peptidoglycan bou
708	31	41.3	1582	2	T15308	hypothetical prote
709	31	41.3	1582	2	AC1153	adhesin homolog, lm
710	31	41.3	1608	1	WMTGM	183K protein - cob
711	31	41.3	1703	2	S15047	SNF2 protein - yea
712	31	41.3	1728	2	T17466	rifamycin polyketi
713	31	41.3	1763	2	T17465	rifamycin polyketi
714	31	41.3	1888	2	T14273	zinc finger protei
715	31	41.3	1888	2	T52022	1-phosphatidylinos
716	31	41.3	2051	2	F66529	probable phosphati
717	31	41.3	2051	2	F66529	transcription factor
718	31	41.3	2183	2	T42764	transcription coac
719	31	41.3	2440	2	S39162	Xin protein - chic
720	31	41.3	2562	2	T14266	translation activa
721	31	41.3	2672	2	A48126	hypothetical prote
722	31	41.3	2685	2	T139755	rifamycin polyketi
723	31	41.3	3113	2	T17467	related to TOM1 pr
724	31	41.3	3839	2	T49799	rifamycin polyketi
725	31	41.3	5069	2	T17464	histone H1 - sea u
726	30.5	40.7	48	1	HSUR1P	histone H1, gonada
727	30.5	40.7	248	1	A4981P	transaldolase (EC
728	30.5	40.7	336	2	A42259	endo-beta-N-acetyl
729	30.5	40.7	339	2	T50159	mitochondrial carr
730	30.5	40.7	371	2	JN0533	finger protein pML
731	30.5	40.7	393	2	T45830	hypothetical prote
732	30.5	40.7	422	2	AB3203	Tn3 family transpo
733	30.5	40.7	502	2	B66372	protein F508.34 [i
734	30.5	40.7	518	2	A84645	probable cytochrom
735	30.5	40.7	527	2	AH2651	probable zinc fing
736	30.5	40.7	554	2	G97433	ABC transporter, m
737	30.5	40.7	571	2	S61131	iron (III) ABC tran
738	30.5	40.7	579	2	T00119	probable membrane
739	30.5	40.7	601	2	T16944	probable transcript
740	30.5	40.7	732	2	T23295	hypothetical prote
741	30.5	40.7	802	2	S43217	ubiquitin-protein
742	30.5	40.7	809	1	T23296	hypothetical prote
743	30.5	40.7	860	2	T33878	hypothetical prote
744	30.5	40.7	1039	2	T40572	hypothetical prote
745	30.5	40.7	1157	2	T39009	protein phosphatas
746	30.5	40.7	1688	2	T26183	hypothetical prote
747	30.5	40.7	2265	2	AD2055	hypothetical prote
748	30	40.0	56	2	A34326	protamine - chicke
749	30	40.0	62	2	T16276	hypothetical prote
750	30	40.0	77	2	AB3643	hypothetical cytos
751	30	40.0	79	2	A13247	hypothetical prote
752	30	40.0	94	2	AB1439	small heat shock p
753	30	40.0	97	2	A11081	a small heat shock
754	30	40.0	100	1	R36G14	ribosomal protein
755	30	40.0	100	1	S78302	ribosomal protein
756	30	40.0	100	2	S76498	ribosomal protein
757	30	40.0	100	2	S36236	wound-induced prot
758	30	40.0	102	2	E75063	hypothetical prote
759	30	40.0	108	2		
760	30	40.0	109	2	E72583	hypothetical prote
761	30	40.0	116	2	C86554	sigma regulatory f
762	30	40.0	116	2	E72069	sigma regulatory f
763	30	40.0	121	2	S27145	gene 30.7 protein
764	30	40.0	122	2	H82231	hypothetical prote
765	30	40.0	128	2	T18104	hypothetical prote
766	30	40.0	130	2	T15423	hypothetical prote
767	30	40.0	135	2	D71168	hypothetical prote
768	30	40.0	136	2	T47982	hypothetical prote
769	30	40.0	139	2	D88955	protein K04F1.9 [i
770	30	40.0	148	2	T37717	hypothetical prote
771	30	40.0	149	2	T25963	hypothetical prote
772	30	40.0	150	2	S27613	hypothetical prote
773	30	40.0	151	2	D83920	Vps homolog - bov1
774	30	40.0	153	2	D83920	hypothetical prote
775	30	40.0	154	2	JQ1137	rRNA methyltransfe
776	30	40.0	154	2	AG0060	probable exported
777	30	40.0	155	2	B95248	hypothetical prote
778	30	40.0	157	2	A72457	hypothetical prote
779	30	40.0	160	2	A48975	Thy-1 glycoprotein
780	30	40.0	164	2	S35220	hypothetical prote
781	30	40.0	166	2	S09224	membrane protein -
782	30	40.0	166	2	S09225	membrane protein -
783	30	40.0	167	2	G71548	hypothetical prote
784	30	40.0	167	2	D82122	hypothetical prote
785	30	40.0	172	2	T12202	probable cdc2-like
786	30	40.0	177	2	A28106	prolactin, 20K - M
787	30	40.0	179	2	F69936	hypothetical prote
788	30	40.0	180	2	AD2467	hypothetical prote
789	30	40.0	181	2	A40607	monofunctional cho
790	30	40.0	185	2	F35719	h1p-like nucleoti
791	30	40.0	185	2	B86104	ATP-binding compon
792	30	40.0	185	2	B91263	ATP-binding compon
793	30	40.0	185	2	AG2026	hypothetical prote
794	30	40.0	192	2	G72712	hypothetical prote
795	30	40.0	193	2	H83356	probable transcrip
796	30	40.0	194	2	PC1136	amidophosphoribosy
797	30	40.0	194	2	T47678	prolactin II precu
798	30	40.0	200	2	B32477	endopeptidase Clp
799	30	40.0	201	2	T07267	late L3 23K protei
800	30	40.0	204	2	S11460	hypothetical prote
801	30	40.0	211	2	A64537	conserved hypotet
802	30	40.0	212	2	B82125	hypothetical prote
803	30	40.0	217	2	H90039	very hypotetrical
804	30	40.0	217	2	T37812	hypothetical prote
805	30	40.0	222	2	B95982	geminin precursor (
806	30	40.0	224	2	B40391	hypothetical prote
807	30	40.0	225	2	A49941	gene 103p protein
808	30	40.0	228	2	S28019	hypothetical prote
809	30	40.0	233	2	AS2073	splicing factor, a
810	30	40.0	238	2	A57198	GCR 101 protein -
811	30	40.0	243	2	S49193	probable pyrroline
812	30	40.0	249	2	G81310	ABC transport prot
813	30	40.0	249	2	C84340	3-oxoacyl-[ACP] re
814	30	40.0	251	2	B82839	hypothetical prote
815	30	40.0	252	2	AC1181	hypothetical prote
816	30	40.0	254	2	AD1538	hypothetical prote
817	30	40.0	254	2	F83282	hypothetical prote
818	30	40.0	258	2	B49597	nonstructural prot
819	30	40.0	258	2	A82874	transcription anti
820	30	40.0	261	2	D64075	ureh protein homol
821	30	40.0	263	2	T34526	hypothetical prote
822	30	40.0	264	2	S66121	vent-1 protein - A
823	30	40.0	268	2	T15693	hypothetical prote
824	30	40.0	274	2	S75896	hypothetical prote
825	30	40.0	282	2	AB1929	hypothetical prote
826	30	40.0	283	2	B83053	dihydropterolate sy
827	30	40.0	283	2	A96655	hypothetical prote
828	30	40.0	287	2	A10782	probable transcrip
829	30	40.0	291	2	F81163	integrase/recombin
830	30	40.0	291	2	C81943	probable integrase
831	30	40.0	294	2	D84338	hypothetical prote
832	30	40.0	296	2	C81906	hypothetical prote

1833	30	40.0	296	2	G81111	conserved hypothe
834	30	40.0	296	2	T47598	hypothetical prote
835	30	40.0	296	2	G84747	Ar-hook DNA-bindin
836	30	40.0	296	2	T35805	hypothetical prote
837	30	40.0	302	1	UN0794	phosphatase butyryl
838	30	40.0	303	2	T43913	DNA gyrase chain B
839	30	40.0	303	2	T43912	DNA gyrase chain B
840	30	40.0	303	2	A83958	integrase/recombin
841	30	40.0	304	2	T38957	probable GPR/FUN34
842	30	40.0	304	2	B75595	conserved hypothe
843	30	40.0	307	2	A39999	hypothetical prote
844	30	40.0	308	2	A83415	integrase (limpote
845	30	40.0	310	2	F82979	probable transcrip
846	30	40.0	311	2	C90049	hypothetical prote
847	30	40.0	312	2	T17118	protein kinase cdc
848	30	40.0	313	1	S70839	ltd homolog - Bra
849	30	40.0	314	2	H82115	probable adenine-s
850	30	40.0	316	2	T09591	probable cdc2-like
851	30	40.0	317	2	G82635	methanol dehydroge
852	30	40.0	321	2	D64820	probable asparagin
853	30	40.0	323	2	A82433	fructokinase VCM06
854	30	40.0	323	2	T01103	probable H+-transp
855	30	40.0	323	2	T45531	agab protein (limp
856	30	40.0	324	1	A41786	mRNA-binding prote
857	30	40.0	325	2	F84740	hypothetical prote
858	30	40.0	325	2	H90204	hypothetical prote
859	30	40.0	326	2	A47493	H+-transporting tw
860	30	40.0	326	2	S50750	dihydrodipicolinat
861	30	40.0	327	2	D84806	hypothetical prote
862	30	40.0	328	2	C69085	DNA repair protein
863	30	40.0	329	2	T47448	sulfotransferase-1
864	30	40.0	330	2	S44160	hypothetical prote
865	30	40.0	330	2	H37366	hypothetical prote
866	30	40.0	332	2	B81743	conserved hypothe
867	30	40.0	333	2	T04656	hypothetical prote
868	30	40.0	333	2	B64380	hypothetical prote
869	30	40.0	335	2	S18143	hypothetical prote
870	30	40.0	337	2	T33957	hypothetical prote
871	30	40.0	340	2	C70741	hypothetical prote
872	30	40.0	340	2	AH0940	probable ABC trans
873	30	40.0	341	2	S60431	hypothetical prote
874	30	40.0	342	2	T46909	hypothetical prote
875	30	40.0	342	2	S57165	hypothetical prote
876	30	40.0	347	2	G86675	carotenoid biosynt
877	30	40.0	348	2	B48435	cysteine proteinas
878	30	40.0	348	2	B82933	type I restriction
879	30	40.0	351	2	A99586	conserved hypothe
880	30	40.0	354	2	T48649	glycerol-3-phospha
881	30	40.0	356	2	AG3612	glycerol kinase (B
882	30	40.0	357	1	HLMS37	MHC class I histoc
883	30	40.0	357	2	T37317	probable Ca2+/calm
884	30	40.0	361	2	F82115	cholesterol synthas
885	30	40.0	361	2	T01007	mannose-1-phosphat
886	30	40.0	362	2	B83542	hypothetical prote
887	30	40.0	364	2	T47698	mannose-1-phosphat
888	30	40.0	364	2	AD2302	hypothetical prote
889	30	40.0	365	2	T38720	heRn - human
890	30	40.0	366	2	C85800	probable cytochrom
891	30	40.0	366	2	G90951	probable cytochrom
892	30	40.0	370	2	F95950	probable ABC trans
893	30	40.0	371	2	H82497	glycerophosphoryl
894	30	40.0	372	1	A55510	cholesterol synthas
895	30	40.0	372	2	P86189	hypothetical prote
896	30	40.0	373	2	T11955	hypothetical prote
897	30	40.0	374	2	G70947	hypothetical prote
898	30	40.0	382	2	A10153	conserved hypothe
899	30	40.0	384	2	A83189	aminopeptidase Atu
900	30	40.0	385	1	T39498	GMP cyclohydrolase
901	30	40.0	388	1	T43899	DNA gyrase chain B
902	30	40.0	391	1	DEUS0	dihydroorotase (EC
903	30	40.0	391	2	S69192	serine O-acetyltra
904	30	40.0	392	2	T32524	hypothetical prote
905	30	40.0	393	2	G71536	hypothetical prote
906	30	40.0	396	2	S27870	house-keeping prot
907	30	40.0	397	2	S43440	3-oxoacyl-CoA thio
908	30	40.0	398	2	T25719	hypothetical prote
909	30	40.0	398	2	B84888	probable methionin
910	30	40.0	398	2	T43225	pheromone receptor
911	30	40.0	399	2	G96690	unknown protein F2
912	30	40.0	401	2	F87641	methionine-gamma-1
913	30	40.0	401	2	H72765	probable flap endo
914	30	40.0	405	2	A86446	unknown protein (i
915	30	40.0	409	2	T31725	hypothetical prote
916	30	40.0	410	2	AD2844	conserved hypothe
917	30	40.0	412	2	A36169	transforming growt
918	30	40.0	413	2	S77371	hypothetical prote
919	30	40.0	414	2	T43415	probable MADS-box
920	30	40.0	414	2	T49459	hypothetical prote
921	30	40.0	414	2	T21954	hypothetical prote
922	30	40.0	416	2	T31785	hypothetical prote
923	30	40.0	419	2	G87293	ornithine decarbox
924	30	40.0	419	2	T48080	translation releas
925	30	40.0	419	2	A86414	hypothetical prote
926	30	40.0	420	2	T39712	hypothetical prote
927	30	40.0	421	2	T52033	13S proteosome sub
928	30	40.0	422	1	SYECFG	tetrahydrofolylpol
929	30	40.0	422	2	AC0802	dihydrofolate synt
930	30	40.0	424	2	B81936	tetrahydrofolylpol
931	30	40.0	424	2	C81170	folypolyglutamate
932	30	40.0	425	2	C96804	hypothetical prote
933	30	40.0	427	2	T42516	hypothetical prote
934	30	40.0	428	2	T46046	hypothetical prote
935	30	40.0	428	2	G89982	hypothetical prote
936	30	40.0	430	2	B82096	conserved hypothe
937	30	40.0	435	2	H82501	nicotinate phospho
938	30	40.0	438	2	T47711	hypothetical prote
939	30	40.0	443	2	B70933	hypothetical prote
940	30	40.0	443	2	T48708	hypothetical prote
941	30	40.0	448	2	F83724	Na+-transporting A
942	30	40.0	448	2	A48939	cellulohydrolase
943	30	40.0	452	1	H65036	CPDdiacylglycerol-
944	30	40.0	452	2	D91060	CPDdiacylglycerol-
945	30	40.0	452	2	B85905	protein kinase (EC
946	30	40.0	454	2	A38643	purine-cytosine pe
947	30	40.0	457	2	E70081	hypothetical prote
948	30	40.0	457	2	T04226	hypothetical prote
949	30	40.0	459	2	H82088	DNA repair protein
950	30	40.0	459	2	G71431	hypothetical prote
951	30	40.0	460	2	G84246	phosphomannomutase
952	30	40.0	460	2	A10078	hypothetical prote
953	30	40.0	461	2	T00621	hypothetical prote
954	30	40.0	462	2	E69070	hydrogenase expres
955	30	40.0	462	2	G01804	interleukin 3-regu
956	30	40.0	466	2	B84535	Ac-like transposas
957	30	40.0	471	2	S57449	fusca protein homo
958	30	40.0	471	2	T20522	hypothetical prote
959	30	40.0	472	2	I57445	alkaline phosphata
960	30	40.0	476	2	A83387	probable mfs dicar
961	30	40.0	477	2	H98235	probable mfs dicar
962	30	40.0	480	2	UC7812	Bcl6 homologous zi
963	30	40.0	483	2	T51068	plastid division p
964	30	40.0	484	2	S53641	protein kinase clk
965	30	40.0	485	2	E83775	aldenhyde dehydroge
966	30	40.0	485	2	T10792	antidiphosphoribosy
967	30	40.0	486	2	S31808	VP5 protein - huma
968	30	40.0	486	2	A89927	VP5 protein - huma
969	30	40.0	488	2	T33626	elastin binding pr
970	30	40.0	488	2	A38728	hypothetical prote
971	30	40.0	491	1	MXXRBF	ribulose-bisphosph
972	30	40.0	491	2	A49597	nonstructural prot
973	30	40.0	491	2	S31784	VP5 protein - bovi
974	30	40.0	491	2	S31783	VP5 protein - bovi
975	30	40.0	491	2	AC1816	hypothetical prote
976	30	40.0	491	2	AC32584	Add-B protein - fr
977	30	40.0	499	2	H86815	hypothetical prote
978	30	40.0	499	2	T49049	hypothetical prote

979	30	40.0	500	2	T40666	acetylglutamate sy
980	30	40.0	500	2	G01646	fusca protein homo
981	30	40.0	506	2	T51702	amidophosphoribos
982	30	40.0	508	2	S74977	hypothetical prote
983	30	40.0	509	2	S64227	hypothetical prote
984	30	40.0	511	2	S52622	amidophosphoribos
985	30	40.0	513	2	B84391	DNA damage-inducib
986	30	40.0	514	2	B87711	coenzyme A transfe
987	30	40.0	517	2	JC7623	protein disulfide-
988	30	40.0	518	2	B48967	anthranilate synth
989	30	40.0	518	2	B24723	anthranilate synth
990	30	40.0	518	2	F70831	probable PPE prote
991	30	40.0	522	2	S75491	hypothetical prote
992	30	40.0	532	2	T06087	epidermal growth f
993	30	40.0	532	2	JC5412	amidophosphoribos
994	30	40.0	533	2	G69140	cobalamin biosynth
995	30	40.0	534	2	T35190	hypothetical prote
996	30	40.0	535	2	B49804	Hsp90 homolog p61
997	30	40.0	540	2	T34187	hypothetical prote
998	30	40.0	548	2	S44654	ZK353.1 protein -
999	30	40.0	552	2	AB2361	hypothetical prote
1000	30	40.0	553	2	T02475	hypothetical prote

ALIGNMENTS

RESULT 1

coagulation factor VIII precursor [validated] - human
 N:Alternative names: antihemophilic factor A; coagulation factor VIIIc; procoagulant compo
 C:Species: Homo sapiens (man)
 C:Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text change 31-Dec-2004
 C:Accession: I54318; A00525; I58059; A23584; A26174; A42348; A43986; S63527; S64445; B42
 R:Gitschler, J.; Wood, W.I.
 Hum. Mol. Genet. 1, 199-200, 1992
 A:Title: Sequence of the exon-containing regions of the human factor VIII gene.
 A:Reference number: I54318; MUID:93265012; PMID:1303178
 A:Accession: I54318
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1921, 'S', 1923-2351 <RES>
 A:Cross-references: UNIPARC:UPI000016A9D3; GB:M88648; NID:g182381; PIDN:
 R:Wood, W.I.; Capon, D.J.; Simonsen, C.C.; Eaton, D.L.; Gitschler, J.; Keyt, B.; Seeburg
 Nature 312, 330-337, 1984
 A:Title: Expression of active human factor VIII from recombinant DNA clones.
 A:Reference number: A00525; MUID:85061548; PMID:6438526
 A:Accession: A00525
 A:Molecule type: mRNA
 A:Residues: 1-2351 <WOO>
 A:Cross-references: UNIPARC:UPI000012A416; EMBL:X01165; EMBL:X01166; EMBL:X01179
 R:Toole, J.J.; Knopf, J.L.; Wozney, J.M.; Sultzman, L.A.; Buecker, J.L.; Pittman, D.D.;
 S. D.N.; Hewick, R.M.
 Nature 312, 342-347, 1984
 A:Title: Molecular cloning of a cDNA encoding human antihemophilic factor.
 A:Reference number: I58059; MUID:85061550; PMID:6438528
 A:Accession: I58059
 A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-74, 'V', 76-1259, 'E', 1261-2351 <RES>
 A:Cross-references: UNIPARC:UPI0000144860; GB:K01740; NID:g182802; PIDN:AAA52484.1; PID:
 R:Trnke, M.A.; Blacher, R.; Burke, D.; Chu, C.; Dina, D.; Hartog, K.; Kuo,
 B.; Randolph, A.; Urdea, M.S.; Valenzuela, P.; Dahl, H.H.; Favallan, J.; Hansen, J.; NC
 DNA 4, 333-349, 1985
 A:Title: Characterization of the polypeptide composition of human factor VIII: C and the
 A:Reference number: A23584; MUID:86081164; PMID:3935400
 A:Accession: A23584
 A:Molecule type: mRNA
 A:Residues: 1-2351 <TRU>
 A:Cross-references: UNIPARC:UPI000012A416; GB:M14113; NID:g182817; PIDN:AAA52485.1; PID:
 R:Batton, D.; Rodriguez, H.; Vehar, G.A.
 Biochemistry 25, 505-512, 1986
 A:Title: Proteolytic processing of human factor VIII. Correlation of specific cleavages

ity.
 A:Reference number: A26174; MUID:86159740; PMID:3082357
 A:Accession: A26174
 A:Molecule type: protein
 A:Residues: 20-36;392-399, 'X', 401-402;1668-1678;1709-1722, 'D', 1723-1725;1741-1755 <BAT>
 A:Cross-references: UNIPARC:UPI0000172296; UNIPARC:UPI0000172297; UNIPARC:UPI0000172298;
 R:Pittman, D.D.; Wang, J.H.; Kaufman, R.U.
 Biochemistry 31, 3315-3325, 1992
 A:Title: Identification and functional importance of tyrosine sulfate residues within re
 A:Reference number: A42348; MUID:92207952; PMID:1554716
 A:Accession: A42348
 A:Molecule type: protein
 A:Residues: 20-36;356-371;392-408;582-594;1668-1669, 'X', 1671;1672-1692;1693-1708;1709-17
 A:Cross-references: UNIPARC:UPI0000172296; UNIPARC:UPI000017229B; UNIPARC:UPI000017229C;
 2A1
 A:Experimental source: recombinant material from Chinese hamster ovary cells
 A:Note: sequence extracted from NCBI backbone and corrected to correspond with the publi
 R:Ray, P.J.; Smudzin, T.M.
 J. Biol. Chem. 264, 14005-14010, 1989
 A:Title: Interubiquitin fluorescence energy transfer in human factor VIII.
 A:Reference number: A43986; MUID:89340500; PMID:2503509
 A:Accession: A43986
 A:Molecule type: protein
 A:Residues: 'X', 517-523;1853-1860, 'X', 1862-1864, 'X', 1866 <RAY>
 A:Cross-references: UNIPARC:UPI00001722A2; UNIPARC:UPI00001722A3
 R:Leyte, A.; van Schijndel, H.B.; Niehrs, C.; Hultner, W.B.; Verbeet, M.P.; Mertens, K.;
 J. Biol. Chem. 266, 740-746, 1991
 A:Title: Sulfation of Tyr(1680) of human blood coagulation factor VIII is essential for
 A:Reference number: A56109; MUID:91093266; PMID:1898735
 A:Contents: annotation; sulfation
 R:Gitschler, J.; Wood, W.I.; Goralaka, T.M.; Wion, K.L.; Chen, E.Y.; Eaton, D.H.; Vehar, 'X'
 Nature 312, 326-330, 1984
 A:Title: Characterization of the human factor VIII gene.
 A:Reference number: A56196; MUID:85061547; PMID:6438525
 A:Contents: annotation; introns
 R:McMullen, B.A.; Fujikawa, K.; Davie, E.W.; Hedner, U.; Ezban, M.
 Protein Sci. 4, 740-746, 1995
 A:Title: Locations of disulfide bonds and free cysteines in the heavy and light chains o
 A:Reference number: A56216; MUID:95338127; PMID:7613471
 A:Contents: annotation; disulfide bonds
 A:Note: 329-Cys, 711-Cys, and 2019-Cys were shown to have free sulfhydryls
 R:Kjálke, M.; Heding, A.; Talbo, G.; Persson, E.; Thomsen, J.; Ezban, M.
 Eur. J. Biochem. 234, 773-779, 1995
 A:Title: Amino acid residues 721-729 are required for full factor VIII activity.
 A:Reference number: S63527; MUID:96163459; PMID:8575434
 A:Accession: S63527
 A:Molecule type: protein
 A:Residues: 733-752;753-759 <KJA>
 A:Cross-references: UNIPARC:UPI00001722A4; UNIPARC:UPI00001722A5
 R:Lind, P.; Larsson, K.; Spira, U.; Sydow-Baackman, M.; Almstedt, A.; Gray, E.; Sandberg
 Eur. J. Biochem. 232, 19-27, 1995
 A:Title: Novel forms of B-domain-deleted recombinant factor VIII molecules. Construction
 A:Reference number: S64445; MUID:96048024; PMID:7556150
 A:Accession: S64445
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1668-1685 <LIN>
 A:Cross-references: UNIPARC:UPI00001722A6
 C:Comment: Factor VIII is activated by factor Xa and thrombin, but prolonged exposure pr
 A:Gene: GDB:R8C
 A:Cross-references: GDB:119124; OMIM:306700
 A:Map position: Xq28-Xq28
 A:Introns: 48/2; 89/1; 130/1; 201/1; 224/1; 263/1; 337/1; 424/2; 481/3; 513/1; 584/3; 63
 C:Function:
 A:Description: acts as a cofactor, with calcium and phospholipid, for the factor IXa pro
 A:Pathway: blood coagulation
 A:Superfamily: coagulation factors V/VIII; disocidin I amino-terminal homology; ferroxid
 C:Keywords: acute phase; blood coagulation; duplication; glycoprotein; hemophilia A; pla
 F1-19/Domain: signal sequence #status predicted <SIG>
 F20-2351/Product: coagulation factor VIII #status experimental <MAT>
 F20-740/Product: coagulation factor VIIIa heavy chain #status experimental <ACH>
 F20-356/Domain: A1 <DNI>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2005, 22:48:32 ; Search time 36.6207 Seconds
(without alignments)
179.972 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect score: 75
Sequence: 1 MSSEPHVLRNRAQSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

A_Geneseq.21: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *
9: Geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	15	7	ADM75918 Human MHC
2	75	100.0	15	7	ADM75967 Human MHC
3	75	100.0	15	7	ADM75952 Human MHC
4	75	100.0	15	7	ADM75974 Human Fac
5	75	100.0	15	8	ADG06422 Human B-d
6	75	100.0	20	5	ABJ05003 A3 pepcid
7	75	100.0	60	5	ABJ04948 A3 domain
8	75	100.0	64	6	ABP60515 Human Fac
9	75	100.0	64	6	ABP60514 Human Fac
10	75	100.0	68	4	AA73022 Human Fac
11	75	100.0	68	4	AA73091 Factor-VI
12	75	100.0	77	3	ADP20767 Factor VI
13	75	100.0	79	5	ADG64594 Recombina
14	75	100.0	128	3	AA807205 Human Fac
15	75	100.0	128	3	AA807205 Factor-VI
16	75	100.0	138	2	AAW33227 Procoagul
17	75	100.0	138	2	AAW33228 Procoagul
18	75	100.0	138	2	AAW33229 Procoagul
19	75	100.0	142	8	ADU47620 Human Fac
20	75	100.0	142	8	ADQ37613 Human Fac
21	75	100.0	142	8	ADQ37598 Human Fac
22	75	100.0	142	8	ADQ37591 Human Fac
23	75	100.0	142	8	ADQ37606 Human Fac
24	75	100.0	142	8	ADU47614 Human fac

25	75	100.0	142	1	AA80268 Modified
26	75	100.0	142	1	AA80268 Modified
27	75	100.0	142	4	AA80268 Modified
28	75	100.0	142	4	AA80268 Modified
29	75	100.0	142	9	AA80267 Modified
30	75	100.0	142	5	AA80267 Modified
31	75	100.0	142	8	ADQ37605 Human Fac
32	75	100.0	142	8	ADQ37590 Human Fac
33	75	100.0	142	8	ADU47612 Human fac
34	75	100.0	142	8	ADQ37599 Human Fac
35	75	100.0	142	8	ADQ37604 Human Fac
36	75	100.0	142	8	ADQ37589 Human Fac
37	75	100.0	142	8	ADQ37614 Human Fac
38	75	100.0	143	8	ADQ37594 Human Fac
39	75	100.0	143	8	ADQ37609 Human Fac
40	75	100.0	143	8	ADQ37600 Human Fac
41	75	100.0	143	8	ADQ37615 Human Fac
42	75	100.0	143	8	ADQ37593 Human Fac
43	75	100.0	143	8	ADQ37608 Human Fac
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98	75	100.0	1656	8	ADU47611	AdU47611	Human	fac	171	75	100.0	2346	2	AAW11391	AAW11391	Active	Pa
99	75	100.0	1661	7	AAW18670	AAW18670	Factor	VI	172	75	100.0	2346	2	AAW11434	AAW11434	Active	Pa
100	75	100.0	2096	8	ADQ39369	ADQ39369	Human	myo	173	75	100.0	2346	2	AAW11351	AAW11351	Active	Pa
101	75	100.0	2098	2	AAW86863	AAW86863	Factor	VI	174	75	100.0	2346	2	AAW11421	AAW11421	Active	Pa
102	75	100.0	2271	8	AAW84598	AAW84598	Human	dia	175	75	100.0	2346	2	AAW11392	AAW11392	Active	Pa
103	75	100.0	2332	2	AAW43257	AAW43257	Human	fac	176	75	100.0	2346	2	AAW11452	AAW11452	Active	Pa
104	75	100.0	2332	2	AAW33224	AAW33224	Procoagul		177	75	100.0	2346	2	AAW11431	AAW11431	Active	Pa
105	75	100.0	2332	2	AAW33225	AAW33225	Procoagul		178	75	100.0	2346	2	AAW11356	AAW11356	Active	Pa
106	75	100.0	2332	2	AAW33222	AAW33222	Procoagul		179	75	100.0	2346	2	AAW11360	AAW11360	Active	Pa
107	75	100.0	2332	2	AAW33226	AAW33226	Procoagul		180	75	100.0	2347	2	AAW11411	AAW11411	Active	Pa
108	75	100.0	2332	2	AAW33223	AAW33223	Procoagul		181	75	100.0	2347	2	AAW11379	AAW11379	Active	Pa
109	75	100.0	2332	2	AAW44132	AAW44132	Human	sapi	182	75	100.0	2347	2	AAW11340	AAW11340	Active	Pa
110	75	100.0	2332	2	AAW53483	AAW53483	Human	fac	183	75	100.0	2347	2	AAW11369	AAW11369	Active	Pa
111	75	100.0	2332	2	AAW31594	AAW31594	Human	fac	184	75	100.0	2347	2	AAW11402	AAW11402	Active	Pa
112	75	100.0	2332	2	AAW57847	AAW57847	Human	fac	185	75	100.0	2348	2	AAW11341	AAW11341	Active	Pa
113	75	100.0	2332	4	AAW10826	AAW10826	Human	mat	186	75	100.0	2348	2	AAW11436	AAW11436	Active	Pa
114	75	100.0	2332	4	AAW50465	AAW50465	Human	fac	187	75	100.0	2348	2	AAW11390	AAW11390	Active	Pa
115	75	100.0	2332	4	AAW71302	AAW71302	N-term	ina	188	75	100.0	2348	2	AAW11409	AAW11409	Active	Pa
116	75	100.0	2332	4	AAW11200	AAW11200	Human	fac	189	75	100.0	2348	2	AAW11378	AAW11378	Active	Pa
117	75	100.0	2332	5	AAU79871	AAU79871	Human	fac	190	75	100.0	2348	2	AAW11449	AAW11449	Active	Pa
118	75	100.0	2332	5	AAU79875	AAU79875	Human	fac	191	75	100.0	2348	2	AAW11386	AAW11386	Active	Pa
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120	75	100.0	2332	5	AAU79870	AAU79870	Human	fac	193	75	100.0	2348	2	AAW11395	AAW11395	Active	Pa
121	75	100.0	2332	5	AAU79872	AAU79872	Human	fac	194	75	100.0	2348	2	AAW11414	AAW11414	Active	Pa
122	75	100.0	2332	5	AAU79874	AAU79874	Human	fac	195	75	100.0	2348	2	AAW11444	AAW11444	Active	Pa
123	75	100.0	2332	5	AAU79873	AAU79873	Human	fac	196	75	100.0	2349	2	AAW11365	AAW11365	Active	Pa
124	75	100.0	2332	6	ABP60513	ABP60513	Human	fac	197	75	100.0	2349	2	AAW11420	AAW11420	Active	Pa
125	75	100.0	2332	7	ADM98117	ADM98117	Human	fac	198	75	100.0	2349	2	AAW11440	AAW11440	Active	Pa
126	75	100.0	2332	8	ADP09122	ADP09122	Human	fac	199	75	100.0	2349	2	AAW11424	AAW11424	Active	Pa
127	75	100.0	2332	8	ADJ92154	ADJ92154	Factor	VI	200	75	100.0	2349	2	AAW11428	AAW11428	Active	Pa
128	75	100.0	2332	8	ADQ71703	ADQ71703	Amino	aci	201	75	100.0	2349	2	AAW11366	AAW11366	Active	Pa
129	75	100.0	2332	8	ADQ37564	ADQ37564	Human	ful	202	75	100.0	2349	2	AAW11401	AAW11401	Active	Pa
130	75	100.0	2332	8	ADR48956	ADR48956	Human	fac	203	75	100.0	2349	2	AAW11355	AAW11355	Active	Pa
131	75	100.0	2332	8	ADR98715	ADR98715	Human	mat	204	75	100.0	2349	2	AAW11373	AAW11373	Active	Pa
132	75	100.0	2332	9	ADM80686	ADM80686	Human	fac	205	75	100.0	2349	2	AAW11338	AAW11338	Active	Pa
133	75	100.0	2332	9	ADM80694	ADM80694	Human	fac	206	75	100.0	2349	2	AAW11430	AAW11430	Active	Pa
134	75	100.0	2332	9	ADM80684	ADM80684	Human	fac	207	75	100.0	2349	2	AAW11443	AAW11443	Active	Pa
135	75	100.0	2332	9	ADM80683	ADM80683	Human	fac	208	75	100.0	2350	2	AAW11375	AAW11375	Active	Pa
136	75	100.0	2332	9	ADM80693	ADM80693	Human	fac	209	75	100.0	2350	2	AAW11376	AAW11376	Active	Pa
137	75	100.0	2332	9	ADM80690	ADM80690	Human	fac	210	75	100.0	2350	2	AAW11380	AAW11380	Active	Pa
138	75	100.0	2332	9	ADM80685	ADM80685	Human	fac	211	75	100.0	2350	2	AAW11358	AAW11358	Active	Pa
139	75	100.0	2332	9	ADM80687	ADM80687	Human	fac	212	75	100.0	2350	2	AAW11359	AAW11359	Active	Pa
140	75	100.0	2332	9	ADM80692	ADM80692	Human	fac	213	75	100.0	2350	2	AAW11379	AAW11379	Active	Pa
141	75	100.0	2332	9	ADM80689	ADM80689	Human	fac	214	75	100.0	2350	2	AAW11405	AAW11405	Active	Pa
142	75	100.0	2332	9	ADM80688	ADM80688	Human	fac	215	75	100.0	2350	2	AAW11413	AAW11413	Active	Pa
143	75	100.0	2332	9	ADM80691	ADM80691	Human	fac	216	75	100.0	2350	2	AAW11413	AAW11413	Active	Pa
144	75	100.0	2332	9	AEK27721	AEK27721	Human	pac	217	75	100.0	2351	1	AAW50059	AAW50059	Human	fac
145	75	100.0	2332	9	AEK11788	AEK11788	Human	pac	218	75	100.0	2351	1	AAW60741	AAW60741	Sequence	
146	75	100.0	2332	9	AEK11784	AEK11784	Human	pac	219	75	100.0	2351	1	AAW81113	AAW81113	Factor	VI
147	75	100.0	2332	9	AEK11787	AEK11787	Human	pac	220	75	100.0	2351	1	AAW80659	AAW80659	Sequence	
148	75	100.0	2332	9	AEK11778	AEK11778	Human	pac	221	75	100.0	2351	2	AAW55352	AAW55352	Sequence	
149	75	100.0	2332	9	AEK11789	AEK11789	Human	pac	222	75	100.0	2351	2	AAW78223	AAW78223	Factor	VI
150	75	100.0	2332	9	AEK11786	AEK11786	Human	pac	223	75	100.0	2351	2	AAW00465	AAW00465	Factor	VI
151	75	100.0	2332	9	AEK11785	AEK11785	Human	pac	224	75	100.0	2351	2	AAW11371	AAW11371	Active	Pa
152	75	100.0	2332	9	AEK11790	AEK11790	Human	pac	225	75	100.0	2351	2	AAW11408	AAW11408	Active	Pa
153	75	100.0	2342	2	AAW11349	AAW11349	Human	pac	226	75	100.0	2351	2	AAW11427	AAW11427	Active	Pa
154	75	100.0	2342	2	AAW11422	AAW11422	Human	pac	227	75	100.0	2351	2	AAW11347	AAW11347	Active	Pa
155	75	100.0	2343	2	AAW11335	AAW11335	Active	Pa	228	75	100.0	2351	2	AAW11445	AAW11445	Active	Pa
156	75	100.0	2343	2	AAW11393	AAW11393	Active	Pa	229	75	100.0	2351	2	AAW11404	AAW11404	Active	Pa
157	75	100.0	2344	2	AAW11432	AAW11432	Active	Pa	230	75	100.0	2351	2	AAW11416	AAW11416	Active	Pa
158	75	100.0	2344	2	AAW11384	AAW11384	Active	Pa	231	75	100.0	2351	2	AAW11352	AAW11352	Active	Pa
159	75	100.0	2344	2	AAW11367	AAW11367	Active	Pa	232	75	100.0	2351	2	AAW11398	AAW11398	Active	Pa
160	75	100.0	2344	2	AAW11410	AAW11410	Active	Pa	233	75	100.0	2351	2	AAW11332	AAW11332	Active	Pa
161	75	100.0	2344	2	AAW11331	AAW11331	Active	Pa	234	75	100.0	2351	2	AAW11399	AAW11399	Active	Pa
162	75	100.0	2344	2	AAW11361	AAW11361	Active	Pa	235	75	100.0	2351	2	AAW11425	AAW11425	Active	Pa
163	75	100.0	2344	2	AAW11370	AAW11370	Active	Pa	236	75	100.0	2351	2	AAW11343	AAW11343	Active	Pa
164	75	100.0	2345	2	AAW11415	AAW11415	Active	Pa	237	75	100.0	2351	2	AAW11362	AAW11362	Active	Pa
165	75	100.0	2345	2	AAW11403	AAW11403	Active	Pa	238	75	100.0	2351	2	AAW11437	AAW11437	Active	Pa
166	75	100.0	2345	2	AAW11348	AAW11348	Active	Pa	239	75	100.0	2351	2	AAW11329	AAW11329	Active	Pa
167	75	100.0	2345	2	AAW11453	AAW11453	Active	Pa	240	75	100.0	2351	2	AAW11377	AAW11377	Active	Pa
168	75	100.0	2345	2	AAW11441	AAW11441	Active	Pa	241	75	100.0	2351	2	AAW11396	AAW11396	Active	Pa
169	75	100.0	2345	2	AAW11383	AAW11383	Active	Pa	242	75	100.0	2351	2	AAW11435	AAW11435	Active	Pa
170	75	100.0	2345	2	AAW11446	AAW11446	Active	Pa	243	75	100.0	2351	2	AAW11387	AAW11387	Active	Pa

244	75	100.0	2351	2	AAW11419	Active Fa	317	75	100.0	2352	2	AAW11450	Active Fa
245	75	100.0	2351	2	AAW11454	Active Fa	318	75	100.0	2352	2	AAW11451	Active Fa
246	75	100.0	2351	2	AAW11496	Factor VI	319	73	97.3	2351	1	AAW10448	Human fac
247	75	100.0	2351	2	AAW10591	Factor VI	320	70	93.3	1014	1	AAW11139	Factor VII
248	75	100.0	2351	2	AAW10590	Factor VI	321	70	93.3	1438	1	AAW10598	Modified
249	75	100.0	2351	2	AAW10592	Factor VI	322	70	93.3	2332	1	AAW17126	Factor VII
250	75	100.0	2351	2	AAW46245	Human fac	323	70	93.3	2332	1	AAW17128	Factor VII
251	75	100.0	2351	2	AAW44373	Human fac	324	70	93.3	2332	1	AAW17127	Factor VII
252	75	100.0	2351	2	AAW21676	Factor VI	325	70	93.3	2332	1	AAW17129	Factor VII
253	75	100.0	2351	3	AAW52537	Human fac	326	70	93.3	2351	2	AAW11461	Active Fa
254	75	100.0	2351	4	AAW48843	Human fac	327	69	92.0	1431	4	AAW67960	Amino aci
255	75	100.0	2351	6	AAO18620	Human fac	328	69	92.0	2343	3	AAW80989	Canine fa
256	75	100.0	2351	6	ABR55803	Human fac	329	69	92.0	2343	3	AAW57846	Canine fa
257	75	100.0	2351	6	ABR99528	Amino aci	330	69	92.0	2351	1	AAW50319	Human ant
258	75	100.0	2351	7	ADK48898	Wild type	331	65	86.7	13	7	ADM75497	Potential
259	75	100.0	2351	7	ADK48895	Wild type	332	64.5	86.0	2352	2	AAW11459	Active Fa
260	75	100.0	2351	7	ADK48899	Wild type	333	64.5	86.0	2352	2	AAW11456	Active Fa
261	75	100.0	2351	7	ADK48898	Wild type	334	64.5	86.0	2352	2	AAW11458	Active Fa
262	75	100.0	2351	7	ADK48896	Wild type	335	64.5	86.0	2352	2	AAW11463	Active Fa
263	75	100.0	2351	7	ADK48894	Wild type	336	64.5	86.0	2352	2	AAW11464	Active Fa
264	75	100.0	2351	7	ADK48893	Wild type	337	64	85.3	13	7	ADM75762	Potential
265	75	100.0	2351	7	ADK48897	Wild type	338	63	84.0	2351	2	AAW11468	Active Fa
266	75	100.0	2351	7	ADM98133	Full-leng	339	63	84.0	2351	2	AAW11472	Active Fa
267	75	100.0	2351	8	ADN49702	Human myo	340	63	84.0	2351	2	AAW11471	Active Fa
268	75	100.0	2351	8	ADQ39371	Human myo	341	60	80.0	2345	2	AAW11466	Active Fa
269	75	100.0	2351	8	ADR98714	Human nat	342	59.5	79.3	320	3	AAW07207	Potential
270	75	100.0	2351	8	ADR92117	Human fac	343	58	77.3	13	7	ADM74968	Potential
271	75	100.0	2351	8	ADU47567	Human fac	344	57	76.0	2349	2	AAW11465	Active Fa
272	75	100.0	2351	8	ADU74378	Human fac	345	56	74.7	16	7	ADM75232	Potential
273	75	100.0	2351	9	ADZ65063	Human fac	346	56	74.7	13	7	AAW49460	Factor VI
274	75	100.0	2351	9	ADZ65059	Human fac	347	56	74.7	41	1	AAW50313	Thrombin
275	75	100.0	2351	9	ADZ65061	Human fac	348	56	74.7	73	3	AAW07206	Human fac
276	75	100.0	2351	9	ADZ65048	Human fac	349	56	74.7	211	1	AAW50091	Truncated
277	75	100.0	2351	9	ADZ65057	Human fac	350	56	74.7	211	1	AAW07203	Human fac
278	75	100.0	2351	9	AE889878	Factor VI	351	56	74.7	868	2	AAW51143	Porcine F
279	75	100.0	2352	2	AAW11337	Active Fa	352	56	74.7	1443	2	AAW44137	Homø bap1
280	75	100.0	2352	2	AAW11353	Active Fa	353	56	74.7	1443	2	AAW31598	Porcine f
281	75	100.0	2352	2	AAW11364	Active Fa	354	56	74.7	1443	4	AAW50469	Porcine f
282	75	100.0	2352	2	AAW11406	Active Fa	355	56	74.7	1467	4	AAE11207	Modified
283	75	100.0	2352	2	AAW11330	Active Fa	356	56	74.7	1467	7	ADD01038	Recombina
284	75	100.0	2352	2	AAW11389	Active Fa	357	56	74.7	1467	7	ADM98132	Porcine F
285	75	100.0	2352	2	AAW11333	Active Fa	358	56	74.7	1467	7	ADM98130	Porcine F
286	75	100.0	2352	2	AAW11345	Active Fa	359	56	74.7	1467	7	ADM98126	HP44/OL F
287	75	100.0	2352	2	AAW11407	Active Fa	360	56	74.7	1467	7	ADM98115	Porcine f
288	75	100.0	2352	2	AAW11429	Active Fa	361	56	74.7	2114	8	ADO71702	Amino aci
289	75	100.0	2352	2	AAW11418	Active Fa	362	56	74.7	2114	8	ADR48955	Porcine f
290	75	100.0	2352	2	AAW11433	Active Fa	363	56	74.7	2114	9	AEA27722	Pig Facto
291	75	100.0	2352	2	AAW11357	Active Fa	364	56	74.7	2115	3	AAW57849	Pig Facto
292	75	100.0	2352	2	AAW11372	Active Fa	365	56	74.7	2133	2	AAW44133	Sue scrof
293	75	100.0	2352	2	AAW11400	Active Fa	366	56	74.7	2133	3	AAW31597	Porcine f
294	75	100.0	2352	2	AAW11447	Active Fa	367	56	74.7	2133	4	AAW50468	Porcine f
295	75	100.0	2352	2	AAW11344	Active Fa	368	56	74.7	2133	4	AAE11203	Porcine f
296	75	100.0	2352	2	AAW11368	Active Fa	369	56	74.7	2133	7	ADK48890	Wild type
297	75	100.0	2352	2	AAW11394	Active Fa	370	56	74.7	2133	7	ADM98113	Porcine f
298	75	100.0	2352	2	AAW11350	Active Fa	371	56	74.7	2347	2	AAW11467	Active Fa
299	75	100.0	2352	2	AAW11354	Active Fa	372	53	71.3	2350	2	AAW11470	Active Fa
300	75	100.0	2352	2	AAW11363	Active Fa	373	52	69.3	2349	2	AAW11460	Active Fa
301	75	100.0	2352	2	AAW11382	Active Fa	374	51.5	68.0	2350	2	AAW11457	Active Fa
302	75	100.0	2352	2	AAW11397	Active Fa	375	51	68.0	13	7	ADM75233	Potential
303	75	100.0	2352	2	AAW11374	Active Fa	376	47.5	63.3	2348	2	AAW11455	Active Fa
304	75	100.0	2352	2	AAW11412	Active Fa	377	47	62.7	14	8	ABW79481	Human fac
305	75	100.0	2352	2	AAW11439	Active Fa	378	45	60.0	13	7	ADM74967	Potential
306	75	100.0	2352	2	AAW11381	Active Fa	379	45	60.0	20	4	ABU05002	A3 pepcid
307	75	100.0	2352	2	AAW11385	Active Fa	380	45	60.0	116	4	AAU64637	Propionib
308	75	100.0	2352	2	AAW11417	Active Fa	381	44	60.0	116	6	ABM61156	Propionib
309	75	100.0	2352	2	AAW11334	Active Fa	382	44	58.7	2347	5	AAW11469	Active Fa
310	75	100.0	2352	2	AAW11336	Active Fa	383	43	57.3	1561	5	ADH48884	NOV70 pro
311	75	100.0	2352	2	AAW11426	Active Fa	384	43	57.3	2304	3	AAW57848	Mouse fac
312	75	100.0	2352	2	AAW11342	Active Fa	385	43	57.3	2319	2	AAW44135	Mus muscu
313	75	100.0	2352	2	AAW11388	Active Fa	386	43	57.3	2319	2	AAW53485	Mutine fa
314	75	100.0	2352	2	AAW11423	Active Fa	387	43	57.3	2319	2	AAW31596	Mouse fac
315	75	100.0	2352	2	AAW11438	Active Fa	388	43	57.3	2319	4	AAW50467	Mouse fac
316	75	100.0	2352	2	AAW11442	Active Fa	389	43	57.3	2319	4	AAE11202	Mutine fa

390	43	57.3	2319	7	ADK48892	Adk48892	Wild type	463	37	49.3	80	4	ABG02132	ABG02132	Novel hum
391	43	57.3	2319	7	ADM98119	Adm98119	Murine fa	464	37	49.3	97	8	ADN21282	ADN21282	Bacterial
392	40	53.3	13	7	ADM5761	Adm5761	Potential	465	37	49.3	102	7	ADE72560	ADE72560	Human end
393	40	53.3	33	1	AAp50318	AAp50318	Peptide e	466	37	49.3	135	5	ADY22596	ADY22596	Plant ful
394	40	53.3	290	7	ABM87660	ABM87660	Rice abio	467	37	49.3	138	5	ABBA9084	ABBA9084	Listeria
395	40	53.3	356	5	ABG91502	ABg91502	Purine/by	468	37	49.3	195	7	ABM73600	ABM73600	DNA clone
396	40	53.3	391	7	ABO79668	ABo79668	Pseudomon	469	37	49.3	197	3	AAAG61029	AAg61029	Arabidops
397	39	52.0	61	5	ABP09722	ABp09722	Human ORF	470	37	49.3	245	4	ABBS58522	ABBS58522	Drosophil
398	39	52.0	83	4	AAU53907	AAu53907	Propionib	471	37	49.3	343	8	ADX71828	ADX71828	Plant ful
399	39	52.0	83	6	ABM50426	ABm50426	Propionib	472	37	49.3	353	8	ADN24650	ADN24650	Bacterial
400	39	52.0	84	8	ADK75097	Adk75097	Plant ful	473	37	49.3	361	6	ABU50323	ABU50323	Protein e
401	39	52.0	86	5	ADK36508	Adk36508	Novel hum	474	37	49.3	362	8	ADN25827	ADN25827	Bacterial
402	39	52.0	131	2	AAV34624	AAy34624	Chlamydia	475	37	49.3	366	6	ABU21594	ABU21594	Protein e
403	39	52.0	161	9	ADY65916	ADy65916	S. mansoni	476	37	49.3	368	8	ADN21892	ADN21892	Bacterial
404	39	52.0	190	4	AAU43382	AAu43382	Propionib	477	37	49.3	369	6	ABU22711	ABU22711	Protein e
405	39	52.0	190	6	ABM39901	ABm39901	Propionib	478	37	49.3	371	6	ABU19941	ABU19941	Protein e
406	39	52.0	208	6	ABR41655	ABr41655	Human DIT	479	37	49.3	375	6	ABU16859	ABU16859	Protein e
407	39	52.0	251	4	AAH70067	AAh70067	Human sec	480	37	49.3	383	6	ABM73109	ABM73109	Staphyloc
408	39	52.0	251	5	ABG65506	ABg65506	Human alb	481	37	49.3	390	7	ABO73986	ABO73986	Pseudomon
409	39	52.0	251	8	ADL78773	Adl78773	Albumin f	482	37	49.3	392	2	AAV21893	AAV21893	PHA beta-
410	39	52.0	314	4	AAH70085	AAh70085	Human sec	483	37	49.3	416	6	ABU19669	ABU19669	Protein e
411	39	52.0	324	4	ABG06360	ABg06360	Novel hum	484	37	49.3	443	4	AAH92694	AAH92694	Human pro
412	39	52.0	405	4	ABG13587	ABg13587	Novel hum	485	37	49.3	445	6	ABU20061	ABU20061	Protein e
413	39	52.0	473	6	ABR58058	ABr58058	Human bes	486	37	49.3	451	7	ADE54766	ADE54766	Rat prote
414	39	52.0	473	6	ABR43181	ABr43181	Human RBM	487	37	49.3	451	8	ADRA46968	ADRA46968	Rat endom
415	39	52.0	562	4	ABG21605	ABg21605	Novel hum	488	37	49.3	459	8	ADX90946	ADX90946	Plant ful
416	39	52.0	744	4	AAH94796	AAh94796	Human pro	489	37	49.3	481	8	ABO59278	ABO59278	Human gen
417	39	52.0	1095	4	ABG21602	ABg21602	Novel hum	490	37	49.3	514	8	ABO59278	ABO59278	Human gen
418	39	52.0	1095	4	ABG21823	ABg21823	Novel hum	491	37	49.3	516	9	ABE28047	ABE28047	Enterobac
419	39	52.0	1261	8	ADG63071	ADg63071	Transcrip	492	37	49.3	525	4	ABH70056	ABH70056	Drosophil
420	39	52.0	1454	7	ADJ69522	ADj69522	Human hea	493	37	49.3	534	7	ADM57332	ADM57332	Human hea
421	39	52.0	1493	6	ABU03484	ABu03484	Angiogene	494	37	49.3	534	7	ADM57332	ADM57332	Recombina
422	39	52.0	1498	6	ABP988434	ABp988434	Human ser	495	37	49.3	553	7	ABO69238	ABO69238	Pseudomon
423	38	51.3	64	6	ABP78434	ABp78434	N. gonorr	496	37	49.3	595	7	ADD14038	ADD14038	Human arc
424	38	51.3	611	3	ABJ32517	ABj32517	S. lavend	497	37	49.3	595	8	ADJ75374	ADJ75374	Marker ge
425	38	51.3	611	7	ABE10289	ABe10289	S. lavend	498	37	49.3	595	9	ADJ06363	ADJ06363	Cyclin-de
426	38	50.7	47	3	ABBS1422	ABBS1422	Human sec	499	37	49.3	595	9	ADZ70496	ADZ70496	Human pro
427	38	50.7	73	7	ADM26040	ADM26040	Hyperther	500	37	49.3	602	4	AAH94639	AAH94639	Human pro
428	38	50.7	137	9	ADV95417	ADv95417	Yeast ubi	501	37	49.3	638	7	ADL15051	ADL15051	Human mal
429	38	50.7	145	9	ADV95419	ADv95419	Yeast ubi	502	37	49.3	666	8	ABM81297	ABM81297	Tumour-as
430	38	50.7	151	7	ABO79467	ABo79467	Pseudomon	503	37	49.3	668	5	ABH98191	ABH98191	Gab2 amin
431	38	50.7	186	3	AAH82472	AAh82472	Yeast APG	504	37	49.3	676	8	ABM81296	ABM81296	Tumour-as
432	38	50.7	223	8	ADY09987	ADy09987	Plant ful	505	37	49.3	676	9	ADY15196	ADY15196	PRO polyP
433	38	50.7	264	8	ADX88933	ADx88933	Plant ful	506	37	49.3	853	4	AAH95413	AAH95413	Human pro
434	38	50.7	302	4	AAH82483	AAh82483	Cotton tr	507	37	49.3	862	6	ABP97756	ABP97756	Amino aci
435	38	50.7	315	8	ADY10878	ADy10878	Plant ful	508	37	49.3	875	6	ABP97756	ABP97756	Amino aci
436	38	50.7	433	6	ABR83623	ABr83623	APG12-GFP	509	37	49.3	886	4	ABBA64308	ABBA64308	Drosophil
437	38	50.7	514	6	AAE30854	AAe30854	P300 prot	510	37	49.3	974	8	ADG42617	ADG42617	Bacterial
438	38	50.7	800	2	AAE30854	AAe30854	Transcrip	511	37	49.3	1037	4	AAH93585	AAH93585	Human pro
439	38	50.7	983	4	ABR70130	ABr70130	Drosophil	512	37	49.3	1037	7	ADF42720	ADF42720	Human MPI
440	38	50.7	2414	2	AAH84882	AAh84882	Transcrip	513	37	49.3	1038	8	ADJ69037	ADJ69037	Human hea
441	38	50.7	2414	2	AAH40057	AAh40057	Cellular	514	37	49.3	1038	8	ADJ75373	ADJ75373	Marker ge
442	38	50.7	2414	2	ABH06340	ABh06340	Human p30	515	37	49.3	1038	8	ADL83112	ADL83112	Human PRO
443	38	50.7	2414	6	ABU03968	ABu03968	Human exp	516	37	49.3	1038	8	ADL14093	ADL14093	Human bar
444	38	50.7	2414	6	ABU03968	ABu03968	Human exp	517	37	49.3	1038	8	ADH14093	ADH14093	Human bar
445	38	50.7	2414	6	ABU03975	ABu03975	Human exp	518	37	49.3	1038	9	ADH40195	ADH40195	Human met
446	38	50.7	2414	6	ABU03975	ABu03975	Human exp	519	37	49.3	1038	9	ADX06361	ADX06361	Cyclin-de
447	38	50.7	2414	6	ABU03976	ABu03976	Human exp	520	37	49.3	1256	8	ADY20444	ADY20444	PRO polyP
448	38	50.7	2441	2	AAH79054	AAh79054	CREB bind	521	37	48.7	90	7	ADP59535	ADP59535	Transcrip
449	38	50.7	2441	2	AAH79054	AAh79054	Cellular	522	37	48.7	102	4	AAH06596	AAH06596	Human foe
450	38	50.7	2441	3	AAH40058	AAh40058	Mouse nuc	523	37	48.7	392	6	ABU28000	ABU28000	Protein e
451	38	50.7	2441	3	AAH40058	AAh40058	Mouse nuc	524	37	48.7	392	6	ABU31880	ABU31880	Protein e
452	38	50.7	2441	4	ABH44555	ABh44555	Mouse wou	525	37	48.7	393	7	ABO65420	ABO65420	Klebsiell
453	38	50.7	2441	6	ABU03977	ABu03977	Human exp	526	37	48.7	394	6	AAU34687	AAU34687	E. coli c
454	38	50.7	2441	8	ADP90352	ADp90352	Mouse CRE	527	37	48.7	394	6	ABU28743	ABU28743	Protein e
455	38	50.7	2441	8	ADP90352	ADp90352	Mouse CRE	528	37	48.7	394	6	ABU28743	ABU28743	Protein e
456	37.5	50.0	388	6	ABU45477	ABu45477	Protein e	529	36	48.0	113	5	ADH75496	ADH75496	Potential
457	37.5	50.0	698	6	ABU16049	ABu16049	Protein e	530	36	48.0	15	5	ABH64580	ABH64580	Human ORF
458	37.5	50.0	698	6	ABU16049	ABu16049	Protein e	531	36	48.0	70	6	AAU59407	AAU59407	Protonib
459	37	49.3	67	2	AAU77529	AAu77529	Staphyloc	532	36	48.0	70	6	ABH55926	ABH55926	Protonib
460	37	49.3	73	4	AAU44285	AAu44285	Protonib	533	36	48.0	91	3	AAH33515	AAH33515	Arabidops
461	37	49.3	73	4	ABM40804	ABm40804	Protonib	534	36	48.0	94	5	ABP10022	ABP10022	Human ORF
462	37	49.3	77	6	AAU46907	AAu46907	Protonib	535	36	48.0	96	3	AAH33829	AAH33829	Arabidops

682	35	46.7	614	8	ADG65458	Novel hum	755	34	45.3	106	7	ADN02550
683	35	46.7	632	8	ADN27275	Bacterial	756	34	45.3	106	7	ADN02546
684	35	46.7	648	8	ADF5109	A. gossypii	757	34	45.3	113	2	AAV76584
685	35	46.7	708	4	ABB61380	Drosophila	758	34	45.3	131	4	AAV75282
686	35	46.7	716	8	ADV89014	Streptococ	759	34	45.3	134	7	ADB65222
687	35	46.7	716	8	ADV80267	Streptococ	760	34	45.3	137	5	ABP00207
688	35	46.7	726	4	AA66716	Human tra	761	34	45.3	138	4	AAU54545
689	35	46.7	726	4	AA030813	Human cel	762	34	45.3	138	6	ABM51064
690	35	46.7	746	8	ADV82390	Streptococ	763	34	45.3	140	3	AA027082
691	35	46.7	849	3	AAV70968	Human Ras	764	34	45.3	147	4	AAU58708
692	35	46.7	913	5	ABP66191	Bifidobac	765	34	45.3	147	6	ABM55227
693	35	46.7	940	3	AAV53040	Human sec	766	34	45.3	149	6	AAU57064
694	35	46.7	940	3	ADK70539	Respirato	767	34	45.3	149	6	ABM53583
695	35	46.7	980	8	ABM82887	Human dia	768	34	45.3	154	4	ABG01354
696	35	46.7	993	9	AEA17265	Mouss gua	769	34	45.3	160	4	AAU55910
697	35	46.7	1011	7	AD663009	Human pro	770	34	45.3	160	7	ABM52429
698	35	46.7	1011	7	AD663013	Human pro	771	34	45.3	162	7	ADB64678
699	35	46.7	1021	7	ABO78659	Pseudomon	772	34	45.3	165	8	ADP81190
700	35	46.7	1078	8	ADS28006	Bacterial	773	34	45.3	166	3	AAH44111
701	35	46.7	1205	6	ABM67325	Phototrab	774	34	45.3	172	4	AAU61439
702	35	46.7	1311	8	ADN23286	Bacterial	775	34	45.3	172	6	ABM57958
703	35	46.7	1596	8	ABH70845	Drosophila	776	34	45.3	185	4	AAU54247
704	35	46.7	1596	8	ADS96464	Drosophila	777	34	45.3	185	6	ABM50766
705	35	46.7	1723	8	AD010059	Novel hum	778	34	45.3	192	8	ABM52896
706	35	46.7	1784	2	AA077223	Tubercous	779	34	45.3	213	4	AAU18651
707	35	46.7	1807	7	ADB85512	Human GIG	780	34	45.3	213	6	ABU97266
708	35	46.7	1807	7	ADC16723	Human mod	781	34	45.3	214	4	AAU17093
709	35	46.7	1807	8	AD018517	Human sof	782	34	45.3	215	4	ADB93801
710	35	46.7	1809	7	AD655015	Rat prote	783	34	45.3	215	4	ABH60881
711	35	46.7	1809	7	AD655009	Rat prote	784	34	45.3	231	7	ADB65411
712	35	46.7	1809	7	AD655006	Rat prote	785	34	45.3	231	9	ADY18931
713	35	46.7	1809	7	AD655012	Rat prote	786	34	45.3	231	9	AEA23724
714	35	46.7	1883	8	ADM87281	Human pro	787	34	45.3	233	6	ABU19678
715	35	46.7	1904	6	ABR57428	Human NOV	788	34	45.3	235	7	ADG10469
716	35	46.7	1911	6	ABU11041	Human pro	789	34	45.3	237	5	AAU69525
717	35	46.7	2496	3	ABH18222	Plaemodu	790	34	45.3	238	4	AAU66845
718	34.5	46.0	392	6	ABU48286	Protein e	791	34	45.3	238	6	ABM63364
719	34.5	46.0	719	3	ABO71502	Pseudomon	792	34	45.3	242	7	ADG14978
720	34.5	46.0	402	4	AAU38284	Salmonell	793	34	45.3	246	8	ADY05015
721	34.5	46.0	406	4	ABH69665	Drosophila	794	34	45.3	256	4	ABG11767
722	34.5	46.0	426	4	AAU34208	Staphyloc	795	34	45.3	262	8	ADP81191
723	34.5	46.0	664	7	ABO82604	Pseudomon	796	34	45.3	273	9	ABM93095
724	34.5	46.0	705	4	AAU36870	Staphyloc	797	34	45.3	275	8	ADU08188
725	34.5	46.0	725	6	ADA55561	Human pro	798	34	45.3	275	9	ADU26409
726	34.5	46.0	819	7	AD646601	Human pro	799	34	45.3	279	8	ADT58215
727	34	45.3	53	4	AAU60249	Protonib	800	34	45.3	282	4	AAU38168
728	34	45.3	53	6	ABM56768	Protonib	801	34	45.3	282	6	ABU47719
729	34	45.3	56	3	AAU02000	Human sec	802	34	45.3	296	7	ADG10467
730	34	45.3	56	4	AAU50827	Protonib	803	34	45.3	299	6	ABU18131
731	34	45.3	56	6	ABM47346	Protonib	804	34	45.3	299	6	ABU18803
732	34	45.3	58	6	ABU24493	Protein e	805	34	45.3	305	4	AAU24766
733	34	45.3	62	4	AAU64471	Protonib	806	34	45.3	305	5	AAU95768
734	34	45.3	62	5	ABP27396	Streptococ	807	34	45.3	305	5	AAU85386
735	34	45.3	62	6	ABM60990	Protonib	808	34	45.3	305	7	ADP85873
736	34	45.3	62	6	ABM60990	Protonib	809	34	45.3	305	8	ADG83510
737	34	45.3	71	4	AAU51209	Human col	810	34	45.3	310	7	ADU19287
738	34	45.3	75	6	ABM47728	Protonib	811	34	45.3	317	8	ADP07851
739	34	45.3	85	3	AAH58503	Lung canc	812	34	45.3	317	4	AAU672194
740	34	45.3	85	4	AAU78985	Human nuc	813	34	45.3	325	7	ADU13489
741	34	45.3	85	7	ADU80579	Nuclear p	814	34	45.3	327	3	AAU43417
742	34	45.3	85	7	ADU80549	imup-2 pr	815	34	45.3	345	6	ABU27701
743	34	45.3	96	2	AAU00330	Human sec	816	34	45.3	347	2	AAU51845
744	34	45.3	96	7	ADD90360	Novel hum	817	34	45.3	351	2	AAU72022
745	34	45.3	96	7	ADG90179	Human pro	818	34	45.3	351	7	ABM89255
746	34	45.3	96	9	ADY25519	Novel hum	819	34	45.3	357	6	ADU11608
747	34	45.3	100	6	ADA54553	Human pro	820	34	45.3	361	6	ABU47621
748	34	45.3	102	3	AAU27084	Zea may	821	34	45.3	362	4	AAU38361
749	34	45.3	104	3	AAU27083	Zea may	822	34	45.3	363	6	ABU39783
750	34	45.3	106	4	AAU78984	Human nuc	823	34	45.3	365	3	AAU606592
751	34	45.3	106	7	ADU80577	Nuclear p	824	34	45.3	365	3	AAU45295
752	34	45.3	106	7	ADU80580	Nuclear p	825	34	45.3	365	8	ADY07252
753	34	45.3	106	7	ADU80576	Nuclear p	826	34	45.3	366	4	ABG01765
754	34	45.3	106	7	ADU80576	Nuclear p	827	34	45.3	371	8	ADU23256
755	34	45.3	106	7	ADU80576	Nuclear p	827	34	45.3	371	8	ADU23256

828	34	45.3	375	2	AAR43664	Aar43664	Ornithine	901	34	45.3	500	2	AAR12770	Aar12770	C1 inhibi
829	34	45.3	375	2	AAR43663	Aar43663	Ornithine	902	34	45.3	500	2	AAR12117	Aar12117	C1 inhibi
830	34	45.3	376	3	AAG06591	Aag06591	Arbido	903	34	45.3	500	2	AAR12769	Aar12769	C1 inhibi
831	34	45.3	376	3	AAG45294	Aag45294	Arbido	904	34	45.3	500	2	AAW18213	Aaw18213	Recombina
832	34	45.3	376	3	AAG45294	Aag45294	Arbido	905	34	45.3	500	2	AAW18213	Aaw18213	Recombina
833	34	45.3	381	8	AD512986	Ad512986	TRICH-9.	906	34	45.3	500	2	AAW18212	Aaw18212	Recombina
834	34	45.3	385	3	AAG45293	Aag45293	Arbido	907	34	45.3	500	2	AAW18207	Aaw18207	Wild-type
835	34	45.3	385	3	AAG48864	Aag48864	Arbido	908	34	45.3	500	2	AAW18216	Aaw18216	Recombina
836	34	45.3	385	3	AAG06080	Aag06080	Arbido	909	34	45.3	500	2	AAW18214	Aaw18214	Recombina
837	34	45.3	385	5	ABP70161	Abp70161	Amino aci	910	34	45.3	500	2	AAW18218	Aaw18218	Recombina
838	34	45.3	385	7	ABM86299	Abm86299	Rice abio	911	34	45.3	500	2	AAW18217	Aaw18217	Recombina
839	34	45.3	385	9	ADY20020	Ady20020	PRO Polyp	912	34	45.3	500	5	ABG76993	Abg76993	Human C1
840	34	45.3	386	3	AAG06590	Aag06590	Arbido	913	34	45.3	500	5	ABG77001	Abg77001	Human C1
841	34	45.3	388	8	ADP99175	Adp99175	Human tra	914	34	45.3	500	5	ABG76995	Abg76995	Human C1
842	34	45.3	392	3	AAG48863	Aag48863	Arbido	915	34	45.3	500	5	ABG76992	Abg76992	Human C1
843	34	45.3	392	3	AAG06079	Aag06079	Arbido	916	34	45.3	500	5	ABG76991	Abg76991	Human C1
844	34	45.3	392	8	ADN21728	Adn21728	Bacterial	917	34	45.3	500	5	ABG76994	Abg76994	Human C1
845	34	45.3	392	8	ADN24482	Adn24482	Bacterial	918	34	45.3	500	7	ADN18724	Adn18724	Human dis
846	34	45.3	393	1	AAW94156	Aaw94156	Beta-keo	919	34	45.3	500	7	ADN58764	Adn58764	Human pro
847	34	45.3	393	1	AAW94156	Aaw94156	Beta-keo	920	34	45.3	500	7	ADN58764	Adn58764	Human pro
848	34	45.3	393	2	AAR10680	Aar10680	Thiolase	921	34	45.3	500	8	ADN91254	Adn91254	Human C1
849	34	45.3	393	2	AAR32191	Aar32191	Sequence	922	34	45.3	500	8	ADN23857	Adn23857	Human C1
850	34	45.3	393	4	AAW71980	Aaw71980	Ralstonia	923	34	45.3	500	9	AEA23540	Aea23540	Human PRO
851	34	45.3	393	6	ADP83240	Adp83240	PhaA with	924	34	45.3	501	8	ADN43281	Adn43281	Bacterial
852	34	45.3	393	6	ADP83240	Adp83240	PhaA with	925	34	45.3	502	9	ABM94194	Abm94194	Human tra
853	34	45.3	394	8	ADN42848	Adn42848	Bacterial	926	34	45.3	513	8	ADJ27205	Adj27205	Human TRI
854	34	45.3	395	6	ABU21267	Abu21267	Protein e	927	34	45.3	517	7	ADN08961	Adn08961	Novel pro
855	34	45.3	395	6	ABU41778	Abu41778	Protein e	928	34	45.3	518	7	ABO74858	AbO74858	Pseudomon
856	34	45.3	398	6	ABU39983	Abu39983	Protein e	929	34	45.3	519	7	ABO74858	AbO74858	Pseudomon
857	34	45.3	408	7	ABM97411	Abm97411	M. xanthu	930	34	45.3	522	5	ABP41513	Abp41513	Human ova
858	34	45.3	409	8	ADN65970	Adn65970	Mouse pro	931	34	45.3	523	3	AAW72229	Aaw72229	Novel
859	34	45.3	409	8	ADN65970	Adn65970	Mouse pro	932	34	45.3	534	7	ADN07878	Adn07878	Novel pro
860	34	45.3	417	4	AAW25777	Aaw25777	Plant ful	933	34	45.3	539	4	ABW58287	Abw58287	Drosophil
861	34	45.3	417	4	AAW75363	Aaw75363	Human sec	934	34	45.3	539	4	ABW58287	Abw58287	Drosophil
862	34	45.3	417	5	AAW74633	Aaw74633	Oestrogen	935	34	45.3	540	3	AAW75930	Aaw75930	Human tra
863	34	45.3	425	8	ADP19164	Adp19164	Human sec	936	34	45.3	544	3	AAW53464	Aaw53464	Human col
864	34	45.3	425	8	ADP73005	Adp73005	Plant ful	937	34	45.3	546	4	ABG10021	Abg10021	Novel
865	34	45.3	433	6	AAW19824	Aaw19824	Human ORF	938	34	45.3	547	8	ABM84720	Abm84720	Human EST
866	34	45.3	433	6	AAW19824	Aaw19824	Human ORF	939	34	45.3	547	8	ABM84720	Abm84720	Human EST
867	34	45.3	434	8	ADY22775	Ady22775	Plant ful	940	34	45.3	547	8	ABM84721	Abm84721	Human dia
868	34	45.3	434	8	ADY09019	Ady09019	Plant ful	941	34	45.3	547	8	ABM84717	Abm84717	Human dia
869	34	45.3	436	6	ABU22367	Abu22367	Protein e	942	34	45.3	547	8	ABM84719	Abm84719	Human dia
870	34	45.3	437	8	ADY11647	Ady11647	Plant ful	943	34	45.3	553	6	ABU19840	Abu19840	Protein e
871	34	45.3	443	8	ADN26405	Adn26405	Bacterial	944	34	45.3	573	3	ABW60673	Abw60673	Drosophil
872	34	45.3	446	3	AAW99670	Aaw99670	Human GMP	945	34	45.3	575	7	ABM89158	Abm89158	Rice abio
873	34	45.3	446	4	AAW93739	Aaw93739	Human pol	946	34	45.3	582	4	AAW91652	Aaw91652	C glutami
874	34	45.3	446	4	AAW93739	Aaw93739	Human pol	947	34	45.3	589	2	AAW01672	Aaw01672	Influenza
875	34	45.3	446	4	ABU52686	Abu52686	Human big	948	34	45.3	589	2	AAW75444	Aaw75444	Influenza
876	34	45.3	446	8	ADJ31676	Adj31676	Human pro	949	34	45.3	589	4	AAW04954	Aaw04954	Influenza
877	34	45.3	446	8	ABM82158	Abm82158	Tumour-as	950	34	45.3	590	9	ABW70991	Abw70991	Human hCA
878	34	45.3	451	6	ABU21586	Abu21586	Protein e	951	34	45.3	602	5	ABW92316	Abw92316	Hericida
879	34	45.3	457	6	ABU44934	Abu44934	Protein e	952	34	45.3	608	9	ABW72330	Abw72330	Segment o
880	34	45.3	459	2	AAW11555	Aaw11555	E. coli al	953	34	45.3	608	9	ABW72330	Abw72330	Segment o
881	34	45.3	460	4	AAU34883	Aau34883	E. coli c	954	34	45.3	610	2	AAW72228	Aaw72228	Mouse fti
882	34	45.3	460	4	AAU38115	Aau38115	Salmonell	955	34	45.3	619	7	ADN12742	Adn12742	Human GPC
883	34	45.3	460	6	ABU48402	Abu48402	Protein e	956	34	45.3	620	8	ADN23006	Adn23006	Human GPC
884	34	45.3	460	6	ABU28887	Abu28887	Protein e	957	34	45.3	636	4	AAU02972	Aau02972	Angiotens
885	34	45.3	460	6	ABU46963	Abu46963	Protein e	958	34	45.3	636	2	AAW72097	Aaw72097	HSV-2 str
886	34	45.3	461	6	AAW39523	Aaw39523	Protein e	959	34	45.3	648	6	ABU35712	Abu35712	Protein e
887	34	45.3	462	8	ADN25462	Adn25462	Bacterial	960	34	45.3	648	6	AAW31274	Aaw31274	Mouse fti
888	34	45.3	466	2	AAW72230	Aaw72230	HSV-2 str	961	34	45.3	685	7	ADG74272	Adg74272	Mouse fti
889	34	45.3	476	2	AAW71323	Aaw71323	Acetyl-Co	962	34	45.3	685	8	ADN29340	Adn29340	Mouse GPC
890	34	45.3	476	2	AAW71323	Aaw71323	Acetyl-Co	963	34	45.3	685	9	ADN15341	Adn15341	Mouse fti
891	34	45.3	476	8	ADP83249	Adp83249	Full leng	964	34	45.3	694	5	AAU74823	Aau74823	Human REP
892	34	45.3	479	8	AAU39195	Aau39195	Protoninb	965	34	45.3	694	5	ABU55903	Abu55903	Human REP
893	34	45.3	479	5	ADN41457	Adn41457	Human CD-	966	34	45.3	694	6	AAW34057	Aaw34057	F2D 8 pro
894	34	45.3	479	6	ABM35714	Abm35714	Human CD-	967	34	45.3	694	7	ADN75320	Adn75320	prostate
895	34	45.3	481	8	AAU02920	Aau02920	Angiotens	968	34	45.3	694	7	ADG74271	Adg74271	Human fti
896	34	45.3	483	8	ABM84716	Abm84716	Human dia	969	34	45.3	694	7	ADN40026	Adn40026	Cancer/fan
897	34	45.3	485	4	AAW41154	Aaw41154	Human pol	970	34	45.3	694	8	ADN87157	Adn87157	Human pro
898	34	45.3	500	2	AAW12771	Aaw12771	C1 inhibi	971	34	45.3	694	8	ADN29339	Adn29339	Human GPC
899	34	45.3	500	2	AAW12772	Aaw12772	C1 inhibi	972	34	45.3	694	8	ADN22266	Adn22266	Human F2D
900	34	45.3	500	2	AAW12773	Aaw12773	C1 inhibi	973	34	45.3	694	8	ADN46693	Adn46693	Cancer-as

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974 34 45.3 694 9 ADX16339 Adx16339 Human fri
975 34 45.3 694 9 AEB28132 Aeb28132 Human fri
976 34 45.3 715 9 ADB65231 Adb65231 Human pro
977 34 45.3 740 2 AAW61533 Aaw61533 Human pas
978 34 45.3 740 4 AAB69149 Aab69149 Human dex
979 34 45.3 740 4 AAU00631 Aau00631 Human dea
980 34 45.3 740 7 AD82732 Human pro
981 34 45.3 740 7 ADJ69474 Human hea
982 34 45.3 740 8 ABM80752 Abm80752 Tumour-as
983 34 45.3 740 9 ADX05576 Adx05576 Cyclin-de
984 34 45.3 741 7 ADM27072 Adm27072 Hyperther
985 34 45.3 751 4 AAG92771 Aag92771 C glutami
986 34 45.3 757 5 ABP66129 Abp66129 Bifidobac
987 34 45.3 777 7 ADM04504 Adm04504 Human pro
988 34 45.3 784 5 ABB93947 Abb93947 Herpicida
989 34 45.3 784 8 ADN73567 Adn73567 Thale cre
990 34 45.3 822 7 ADD13667 Add13667 C. gluram
991 34 45.3 890 4 ABG08340 Abg08340 Novel hum
992 34 45.3 905 8 ADQ08724 Adq08724 Clona int
993 34 45.3 906 9 AEB53801 Aeb53801 Drosophi1
994 34 45.3 934 9 ADY60907 Ady60907 Abiotic s
995 34 45.3 940 8 ADF42722 Adf42722 Mouse mp1
996 34 45.3 1025 7 ADR06827 Adr06827 Bacterial
997 34 45.3 1072 7 ADC83636 Adc83636 LTRPC3-re
998 34 45.3 1072 8 ADI93477 Adi93477 Murine tr
999 34 45.3 1106 8 ADL82993 Adl82993 Human PRO
1000 34 45.3 1106 9 ADY14329 Ady14329 PRO polyP
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ALIGNMENTS

RESULT 1

ADM75918 ADM75918 standard; peptide; 15 AA.

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XX AC ADM75918;
XX DT 03-JUN-2004 (first entry)
XX DE Human MHC class II binding human Factor VIII peptide G.
XX KW human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
XX KM MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.
XX OS Homo sapiens.
XX PN WO2003087161-A1.
XX PD 23-OCT-2003.
XX PF 17-APR-2003; 2003WO-EP004063.
XX PR 18-APR-2002; 2002EP-00008712.
XX PS 24-MAR-2003; 2003EP-00006554.
XX PA (MERE ) MERCK PATENT GMBH.
XX PI Jones T, Baker M, Carr FJ;
XX DR WPI; 2003-845307/78.
XX PT New modified human Factor VIII molecule being substantially non-
XX PT immunogenic or less immunogenic than non-modified human Factor VIII,
XX PT useful in preparing a composition for treating e.g., Gaucher's disease.
XX PS Disclosure; Page 10; 68pp; English.
XX CC The invention relates to a novel modified human Factor VIII molecule. The
XX CC modified human Factor VIII molecule being substantially non-immunogenic
XX CC less immunogenic than a non-modified human Factor VIII and having
XX CC essentially the same biological specificity and activity when used in
XX CC vivo. The modified human Factor VIII molecule comprises specifically
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CC altered amino acid residues compared with the non-modified parental
CC molecule, where the altered amino acid residues cause a reduction or an
CC elimination of one or more of the T-cell epitopes, which act in the
CC parental non-modified molecule as MHC class II binding ligands and
CC stimulate T-cells. The potential MHC class II binding activity peptide is
CC useful for the manufacture of the modified Factor VIII molecule or a
CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.
CC The modified Factor VIII molecule is useful in preparing a composition
CC for treating e.g., Gaucher's disease. This sequence represents a human
CC Factor VIII peptide with potential human MHC class II binding activity of
CC the invention.
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SQ Sequence 15 AA;

Query Match 100.0%; Score 75; DB 7; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSSSPHYLRNRAQSG 15

Db 1 MSSSPHYLRNRAQSG 15

RESULT 2

ADM75967 ADM75967 standard; peptide; 15 AA.

```
XX AC ADM75967;
XX DT 03-JUN-2004 (first entry)
XX DE Human MHC class II binding human Factor VIII proliferative peptide #45.
XX KW human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
XX KM MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.
XX OS Homo sapiens.
XX PN WO2003087161-A1.
XX PD 23-OCT-2003.
XX PF 17-APR-2003; 2003WO-EP004063.
XX PR 18-APR-2002; 2002EP-00008712.
XX PS 24-MAR-2003; 2003EP-00006554.
XX PA (MERE ) MERCK PATENT GMBH.
XX PI Jones T, Baker M, Carr FJ;
XX DR WPI; 2003-845307/78.
XX PT New modified human Factor VIII molecule being substantially non-
XX PT immunogenic or less immunogenic than non-modified human Factor VIII,
XX PT useful in preparing a composition for treating e.g., Gaucher's disease.
XX PS Disclosure; Page 20; 68pp; English.
XX CC The invention relates to a novel modified human Factor VIII molecule. The
XX CC modified human Factor VIII molecule being substantially non-immunogenic
XX CC or less immunogenic than a non-modified human Factor VIII and having
XX CC essentially the same biological specificity and activity when used in
XX CC vivo. The modified human Factor VIII molecule comprises specifically
XX CC altered amino acid residues compared with the non-modified parental
XX CC molecule, where the altered amino acid residues cause a reduction or an
XX CC elimination of one or more of the T-cell epitopes, which act in the
XX CC parental non-modified molecule as MHC class II binding ligands and
XX CC stimulate T-cells. The potential MHC class II binding activity peptide is
XX CC useful for the manufacture of the modified Factor VIII molecule or a
XX CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.
XX CC The modified Factor VIII molecule is useful in preparing a composition
XX CC for treating e.g., Gaucher's disease. This sequence represents a human
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